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Organization
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1/21, C07K 14/32 Krogshøjvej 36, DK-2880 Bagsværd (DK).
- (21) International Application Number: PCT/DK2003/000200
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- (71) Applicant (for all designated States except US): NOVOZYMES A/S [DK/DK]; Krogshøjvej 36, DK-2880 Bagsværd (DK).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): ANDERSEN, Jens, Tønne [DK/DK]; Alfred Christensens Vej 35, DK-2850 Nærum (DK). JØRGENSEN, Steen, Troels [DK/DK]; Prunusvej 5, DK-3450 Allerød (DK). RASMUSSEN, Michael, Dolbjerg [DK/DK]; Syvhøjvænge 151, DK-2625 Vallensbæk (DK). OLSEN, Peter, Bjarke [DK/DK]; Svendborggade 8, 4 tv, DK-2100 Copenhagen Ø (DK). CLAUSEN, Ib, Groth [DK/DK]; Fyrrestien 6, DK-3400 Hillerød (DK).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2003/087148 A3

(54) Title: BACILLUS LICHENIFORMIS MUTANT HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell comprising a mutation (deletion) in one or more genes encoding polypeptides involved in sporulation wherein the mutant host cell expresses at least 5% less of the one or more polypeptides involved in sporulation than the parent host cell, when cultivated under comparable conditions. The mutant host cell is used for producing heterologous polypeptides.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 03/00200

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/75 C12N1/21 C07K14/32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 03185 A (NOVONORDISK AS ;PRIEST FERGUS G (GB); FLEMING ALASTAIR B (GB); TAN) 30 January 1997 (1997-01-30) the whole document --- X FLEMING A B ET AL: "Extracellular enzyme synthesis in a sporulation-deficient strain of <i>Bacillus licheniformis</i> ." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 61, no. 11, November 1995 (1995-11), pages 3775-3780, XP002902964 ISSN: 0099-2240 abstract --- X WO 98 22598 A (NOVO NORDISK BIOTECH INC) 28 May 1998 (1998-05-28) page 6, line 8 - line 11; claims 1,2,17 ---	1-21 1-21 1-21
		-/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

° Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

15 July 2003

Date of mailing of the international search report

28. 10. 2003

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Ida Christensen

INTERNATIONAL SEARCH REPORT

Interr Application No
PCT/DK 03/00200

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 02 00907 A (JOERGENSEN STEEN TROELS ; OLSEN CARSTEN (DK); NOVOZYMES AS (DK); AN) 3 January 2002 (2002-01-03) claims -----	6,7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 03/00200

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-21 (partially)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 2.

Invention 2 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 4.

Invention 3: claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 6

Invention 4 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No:

etc....
etc....
etc....

Invention 96 :claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 191.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/DK 03/00200

Patent document cited in search report	Publication date		Patent family member(s)		Publication date
WO 9703185	A 30-01-1997		AU 6353896 A CN 1190434 A WO 9703185 A1 EP 0837925 A1 JP 11509096 T		10-02-1997 12-08-1998 30-01-1997 29-04-1998 17-08-1999
WO 9822598	A 28-05-1998		AT 246251 T AU 5445098 A DE 69723855 D1 EP 0941349 A1 JP 2001503641 T WO 9822598 A1 US 5958728 A		15-08-2003 10-06-1998 04-09-2003 15-09-1999 21-03-2001 28-05-1998 28-09-1999
WO 0200907	A 03-01-2002		AU 6583501 A CN 1437656 T WO 0200907 A1 EP 1297170 A1 US 2003032186 A1		08-01-2002 20-08-2003 03-01-2002 02-04-2003 13-02-2003

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attttgattt ctcaaggaac gcacattaga cgaatgccca gcataggata atacgaggaa		480
aaacaaggag gcatgaccga atg tct gaa tac agg gaa att atc act aaa gcg		533
Met Ser Glu Tyr Arg Glu Ile Ile Thr Lys Ala		
1 5 10		
gtg gtc gcg aaa ggc cgg aaa ttc acc cag tcc act cat aca atc tcc		581
Val Val Ala Lys Gly Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser		
15 20 25		
cct tcg caa aag cca acc agt att tta ggc ggt tgg att atc aat cat		629
Pro Ser Gln Lys Pro Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His		
30 35 40		
aag tat gac gct gaa aaa atc gga aaa acc gtg gaa att gaa ggg aca		677
Lys Tyr Asp Ala Glu Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr		
45 50 55		
tat gat atc aac gtc tgg tat tca tat gcg gac aac acc aaa acc gaa		725
Tyr Asp Ile Asn Val Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu		
60 65 70 75		
gtt gtg aca gaa cgc gtt tcc tat gtt gat gtc att aag ctc cgg tat		773
Val Val Thr Glu Arg Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr		
80 85 90		
cgc gac aaa aat tac tta gat gat gaa cac gaa gtc att gcg aaa gtc		821
Arg Asp Lys Asn Tyr Leu Asp Asp Glu His Glu Val Ile Ala Lys Val		
95 100 105		
ctt cag cag ccg aac tgc ctt gaa gtg acc att tct ccg aac gga aac		869
Leu Gln Pro Asn Cys Leu Glu Val Thr Ile Ser Pro Asn Glu Asn		
110 115 120		
aaa gtg gtt gta cag gcg gaa aga gaa ttt tta gca gag gtc gtc ggc		917
Lys Val Val Val Gln Ala Glu Arg Glu Phe Leu Ala Glu Val Val Glu		
125 130 135		
gag acg aag gtc gtc gtt gag gtc aat tct gat tgg acg gaa agc gat		965
Glu Thr Lys Val Val Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp		
140 145 150 155		
gaa gaa gaa gcg tgg gaa gaa gag ctt gat gaa gaa ctt gag gat atc		1013
Glu Glu Glu Ala Trp Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile		
160 165 170		
aat ccc gag ttt ttg gtt gga gat cca gaa gaa taaaaggaag ctagggaaac		1066
Asn Pro Glu Phe Leu Val Gly Asp Pro Glu Glu		

10295.204.ST25.txt

175

180

accggccctag tttctttttt ttcagcacga atctttatgg tataatgagt gttggaatca	1126
atagaaacgt ttatacatag tgagggatta aatatggcag gctacacgc tatacgat	1186
caatatttaa agattaaggc agagtatcgat gatgcctttt tatttttcg tcttggcgc	1246
ttttatgaga tgtttttgta agatgaaaaa aaggcgtctc aggagctcg aatcacfctg	1306
acgagcaggc acggaggatc aagcgaaaaga attccgatgt gcggggttcc ttatcattcc	1366
tgctcttcgt atatcgaca gctcattaaa aaaggctata aagtcgcgt ctgtgaacag	1426
gtggaggacc ctaaatcggc caaaggagtc gtcaaaaagg aagtcgtcgca gctgatcaca	1486
ccggcaccg tcatggacgg caaaggattt catgaaaaatg aaaacaactt tatcgctct	1546
gtc	1549

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<211> 182

<212> PRT

<213> *Bacillus licheniformis*

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Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser Pro Ser Gln Lys Pro		
20	25	30

Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His Lys Tyr Asp Ala Glu		
35	40	45

Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val		
50	55	60

Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg			
65	70	75	80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr		
85	90	95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn		
100	105	110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln		
115	120	125

Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val		
130	135	140

Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp			
145	150	155	160

10295.204.ST25.txt

Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile Asn Pro Glu Phe Leu
165 170 175

Val Gly Asp Pro Glu Glu
180

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<213> *Bacillus licheniformis*

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	tctttattct aacataaggtaaaatcgcaa gtaaaacgat cataaggctt gaaagcgagc	180
	aatgttcca tgtgaaacag tgtcagtcga gaaacccga tttttcttta tttttcttc	240
	tcgccttct gatcagcaac aatataatca aaactgcgac cagaagcgtc acgcgaagcc	300
	ctccgctcaa aaatagaaaa aagtccctca acatatccaa cacattgatc acctctca	360
	gttgtcaattt agatgcaaaa atcccgattt atttgacttc ccctttccaa aacggtctaa	420
	aacgtccctc agattcttct taaccttag acggtaatgg gcataatgctg actaagaaaa	480
	agcaataaaag gagaatatga atg aca aca aaa aca ttg gct tgg cat gaa acg	533
	Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr	
1	5	10

ttg gag ttg cat gaa cta atc gcg gca cag tct gtc gga ttg gtg aag
 Leu Glu Leu His Glu Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys
 15 20 25 581

atc aag aaa agc atg aag aaa atc agc gac cct cag tta aga cag ctt
Ile Lys Lys Ser Met Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu
30 35 40

tac agc gtg tca gca aaa gca ttg gag caa aat tta aga gag ctt ctt
 Tyr Ser Val Ser Ala Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu
 45 50 55

gac ttg tat ttt gat gcg ggt gat ctg ttg gtg ctg gcg aaa acg acc
Asp Leu Tyr Phe Asp Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr
80 85 90

gtt cga aac tat gcg att gcg atc acg gaa acg gcg acg ccc gag ctc
 Val Arg Asn Tyr Ala Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu
 95 100 105

agg	aga	gtg	ctt	gtt	aaa	caa	atc	aat	gcg	gcc	att	aag	ttg	cat	gaa
Arg	Arg	Val	Leu	Val	Lys	Gln	Ile	Asn	Ala	Ala	Ile	Lys	Leu	His	Glu
		110				115						120			

caa gtt ttt tat ttt atg tac caa aga ggc tta tat ccc gcc tat aac 917
Page 11

10295.204.ST25.txt

Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn
 125 130 135

ctc gtc gac ctg cta aaa ggc gac gcc atg cat gcg caa aaa gcg ata 965
 Leu Val Asp Leu Leu Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile
 140 145 150 155

tcg atg aga taaaaaaagcc agcgaggata gaatcctcac tggctctgtt 1014
 Ser Met Arg

tttgctatt ttacgattaa aaccggacac ttcaactcttt tcgccacttt atggctgaca 1074
 cttccgagca ccatttcctg caaagtgttc agccccctgc ttccgataat cacgatatca 1134
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<210> 10
 <211> 158
 <212> PRT
 <213> Bacillus licheniformis

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 20 25 30

Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala
 35 40 45

Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys
 50 55 60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp
 65 70 75 80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala
 85 90 95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val
 100 105 110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe
 115 120 125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu
 Page 12

10295.204.ST25.txt

130

135

140

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg
 145 150 155

<210> 11
 <211> 1752
 <212> DNA
 <213> *Bacillus licheniformis*

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 <222> (183)..(1256)

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acatacgcgc	cgtaaagaca	agtgtactga	ggcaaatgac	tgttttgtt	caaacttagg	180
cggctcgctt	ccgggacagg	ttttttcac	atatgatatg	tcagctgaaa	aaggaggaaa	227
tg atg atg agt	gcc act gcc	ttg ccg	gcc ttt agg	ctg cac att	cat	
Met Met Ser Ala	Thr Ala Leu Pro	Ala Phe Arg	Leu His Ile His			
1	5	10	15			
ccg aag cat ctg	ctt gag ttg	aaa gac gtc	tgg agt gat	gaa gcc	275	
Pro Lys His Leu	Leu Glu Leu Lys	Lys Asp Val Trp	Ser Asp Glu Ala			
20	25	30				
gtt ccc ggc atg	ctc ttg acc	ggt tca gca	aag acg	cct gtc gca gtg	323	
Val Pro Gly Met	Leu Leu Thr Gly	Ser Ala Lys	Thr Pro Val	Ala Val		
35	40	45				
tca tac aga ggg	gcc cac cgc	aaa ctg acg	aaa aaa tcc	tat ttc	371	
Ser Tyr Arg Gly	Ala His Thr Arg	Lys Leu Thr Lys	Ser Tyr Phe			
50	55	60				
att caa tat ccg	gac aat aaa gaa	aag gct gcg	ttt cat ttg	aac gcc	419	
Ile Gln Tyr Pro	Asp Asn Lys	Glu Lys Ala	Ala Phe His	Leu Asn Ala		
65	70	75				
gaa tat cat gat	ccg tct ttc	atc aga aac	agg ctt tcc	ttt cat ttt	467	
Glu Tyr His Asp	Pro Ser Phe	Ile Arg Asn	Arg Leu Ser	Phe His Phe		
80	85	90	95			
ttt gaa caa atc	ggc gtc ctt	gcg cca gca	gca tca cac	gtt ttc ctt	515	
Phe Glu Gln Ile	Gly Val Leu Ala	Pro Ala Ala	Ser His Val	Phe Leu		
100	105	110				
tat atc aat gaa	aaa aaa gaa ggc	atc tat tta	aaa atc gaa	tct gtt	563	
Tyr Ile Asn Glu	Lys Lys Glu Gly	Ile Tyr Leu Lys	Ile Glu Ser Val			
115	120	125				
gac gat cat ttc	tta aag agg aga	aat tta gaa agg	ggg gcc att	tat	611	
Asp Asp His Phe	Leu Lys Arg Arg	Asn Leu Glu Arg	Gly Ala Ile Tyr			
130	135	140				
tat gcc gtt gat	gac gat gct	aat ttt tct	ctg ctg	agt tcc ttc aat	659	
Tyr Ala Val Asp	Asp Asp Ala Asn	Phe Ser Leu	Leu Ser Ser	Phe Asn		
145	150	155				
aaa aag gct aag	caa aat ctc atg	cag gga tac	gaa aga aaa acg	ggt	707	
Lys Lys Ala Lys	Gln Asn Leu Met	Gln Gly Tyr	Glu Arg Lys Thr	Gly		
160	165	170	175			

10295.204.ST25.txt

tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat Ser Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn 180 185 190	755
acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp 195 200 205	803
gtc aaa caa tat ttg ctg tgg ctc atc ggc gtc tgc acc caa aat Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn 210 215 220	851
ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr 225 230 235	899
aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cg Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg 240 245 250 255	947
aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly 260 265 270	995
tat aat acg ctg tct gca agg ctg ctc gac atc ccg gct ttt caa tcc Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser 275 280 285	1043
caa tac ttt aat tta atg aaa aat gtc ttg cac cgc caa ttt aca atc Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile 290 295 300	1091
agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro 305 310 315	1139
ttt ctt gaa cat gat cct tat aca acc gtc aca tac agc cgg ctc gaa Phe Leu Glu His Asp Pro Tyr Thr Val Thr Tyr Ser Arg Leu Glu 320 325 330 335	1187
gat gag caa aaa caa att ttt cat ttc atc gat cag agg aag cgg ttc Asp Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe 340 345 350	1235
ctg ctt ttc gag ctt tcc cga taatagactg tcgctgtcct ccgaaaaaaaa Leu Leu Phe Glu Leu Ser Arg 355	1286
tgtcacattt tttgtcatat tggcgaaaaa aatccctttt acacaaaata aggtatacta gcaatatcaa ggacatcaat gcgcgtgaata cctgaaatta ccgactcaa atacaaatcg aaagttggag actgccatga tgaacaataa aattgaagca aaaagactgg ccttatttga agctgccgaa aagttcggca tcaactccaa agaggccatt cgatgcagtc aggaatttgg caacttgctg aatcaaagaa tgcaaaagga tgataactgc gtgcgtgcgg aagaaagaaa aggccgccac acgtcatgac ctccgactgc aagctgcgcc tgatgccggc ctcccttc ctccatttca tcatccgttg atttcgggtc gcagcttggg ctattcggcc attgttttt gaacataaat catcgtgcaa ataccgttagg caagaatggc tgaagg	1346 1406 1466 1526 1586 1646 1706 1752

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<211> 358
<212> PRT

10295.204.ST25.txt

<213> Bacillus licheniformis

<400> 12

Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His Pro
1 5 10 15

Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala Val
20 25 30

Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val Ser
35 40 45

Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
50 55 60

Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu
65 70 75 80

Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe
85 90 95

Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr
100 105 110

Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp
115 120 125

Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr
130 135 140

Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys
145 150 155 160

Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser
165 170 175

Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr
180 185 190

Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val
195 200 205

Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe
210 215 220

Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys
225 230 235 240

Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn
245 250 255

10295.204.ST25.txt

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr
 260 265 270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln
 275 280 285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser
 290 295 300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe
 305 310 315 320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp
 325 330 335

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 340 345 350

Leu Phe Glu Leu Ser Arg
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cagtttccc cgatggaggc gctgaaaaaa gggacgcttt ggccgtatt ttacgatcat	180
tatgaaaatc cgtatgaaga tgggaggtaa ggagggtgac gaactctta ccgcaagact	240
attataaaag gcttcatgaa attcaggctg ttgatttgt catcgttgag ctgatgctat	300
accttgacac acatcccgat gataccgatg ccatcaaaca atacaaccag tatgccggat	360
tttccagaaa actgaaagcg aagttgaat caaaaatacgg ccctttgatt caaggaagcc	420
cggatcagac ggaatcctat tggagctgga aaagaagtcc ttggccatgg caagttaat	480
agaggaaggg agtcaggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct	533
Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro	
1 5 10	

gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag	581
Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu	
15 20 25	

caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg	629
Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Leu Arg Tyr Leu	
30 35 40	

aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac	677
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10295.204.ST25.txt

Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp
 45 50 55

atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta 725
 Ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val
 60 65 70 75

tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg 773
 Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly
 80 85 90

ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac 821
 Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn
 95 100 105

gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat 869
 Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp
 110 115 120

ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa gcg agg 917
 Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg
 125 130 135

gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat 965
 Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn
 140 145 150 155

gac ggg ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc 1013
 Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg
 160 165 170

tcc cgc gaa gct gtc gaa att ttg aag gaa gag cgc gac cgt aaa aaa 1061
 Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys
 175 180 185

gtg ttt taaaacagcaa aaagccgaaa atacgaccgt attttcggct ttttattttac 1117
 Val Phe

tgcaccgggc tcgcaaggcag ttctgctgcg cggtcgcgca gcacatattt ttgaactttt 1177

ccggatgcgg tcagcgggta ttctgcgatc agaaatacgt actccggaat tttataatac 1237

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catttaataa aggcagccgt ttttccccg tactttcat ccggAACGCC gacaacctgt 1357

acatcgacaa tattcctcatg ttccataaagg aattcctcta tttcacgcgg gttaatgttt 1417

tccccggcgc ggacgatcat atctttaag cggccggtaa tcctcacgta tccgtccccg 1477

tccatttctg ccaaattctcc ggtatggagc cagccgtctt catcgatggc ctttttgtg 1537

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<211> 189

<212> PRT

<213> *Bacillus licheniformis*

<400> 14

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Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu Gln Tyr Gly Gly Ala
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20

10295.204.ST25.txt

25

30

Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu Asn Gln Arg Tyr Ser
 35 40 45

Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp Ile Gly Thr Glu Glu
 50 55 60

Phe Ala His Leu Glu Met Ile Ala Thr Met Val Tyr Lys Leu Thr Lys
 65 70 75 80

Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr
 85 90 95

Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn Ala Ala Gly Val Pro
 100 105 110

Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp Pro Ile Ala Asp Leu
 115 120 125

Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp
 130 135 140

Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn Asp Gly Leu Ala Phe
 145 150 155 160

Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg Phe Arg Glu Ala Val
 165 170 175

Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys Val Phe
 180 185

<210> 15
 <211> 1241
 <212> DNA
 <213> *Bacillus licheniformis*

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 <222> (519)..(1028)

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aaatcgggga gtaaccagcg ataaagttcg gacgctctca	gaagaagaaa aagaaaatat
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aaaagcagcc gcaccgaatgaaaaaggac	aaagagagaa aagaacgctg atgcgtcatc
agaaaaatggc gagagaccaa	gagaaaaact
gaagaagaag aaacagaaca	aatagactga
tcgacaacgg agggagcaag	gagaaaaact
aaaacacagc aacagcggaa	420
aattcaaccc agtcagatac	

10295.204.ST25.txt

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acaacattta ataatagtaa atggaaggag gaaaagaa atg gaa aca aga cca tat Met Glu Thr Arg Pro Tyr	536
1 5	
tca tgg att gcg ctt gac ccg gaa tgc gaa cat cca ggc aac gat tat Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu His Pro Gly Asn Asp Tyr	584
10 15 20	
cac cct agt tat cct aag aaa aaa tta tgt gac gac tat act tgc aac His Pro Ser Tyr Pro Lys Lys Lys Leu Cys Asp Asp Tyr Thr Cys Asn	632
25 30 35	
tgt ggt agg aaa ggg caa aat ggc ttt atc gat tct gac cta gat caa Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile Asp Ser Asp Leu Asp Gln	680
40 45 50	
ctt cat ctt aac aaa cag ctc tca gat gaa acg atc atc att aaa gac Leu His Leu Asn Lys Gln Leu Ser Asp Glu Thr Ile Ile Ile Lys Asp	728
55 60 65 70	
tct tgt gat gtt caa gtc tca act gaa gac aca caa acg ttg gca tca Ser Cys Asp Val Gln Val Ser Thr Glu Asp Thr Gln Thr Leu Ala Ser	776
75 80 85	
gtc atg aca gct gca caa aca cta gct gtt act att att ctc gcc att Val Met Thr Ala Ala Gln Thr Leu Ala Val Thr Ile Ile Leu Ala Ile	824
90 95 100	
atc gat gat cct gat cta gcc gaa ctt gtc aca act gat ctg ttg cag Ile Asp Asp Pro Asp Leu Ala Glu Leu Val Thr Thr Asp Leu Leu Gln	872
105 110 115	
gta act gcc aat aaa caa acg aac aga caa aaa ttg gtg atc gat aat Val Thr Ala Asn Lys Gln Thr Asn Arg Gln Lys Leu Val Ile Asp Asn	920
120 125 130	
tcc aga aat gta cat gtc aca acc gaa gat aca gac aca gct atc atc Ser Arg Asn Val His Val Thr Glu Asp Thr Asp Thr Ala Ile Ile	968
135 140 145 150	
gta agc aca ttt gtt caa act gtt gta atc acc atc acc gcc ctt atc Val Ser Thr Phe Val Gln Thr Val Val Ile Thr Ile Thr Ala Leu Ile	1016
155 160 165	
gtc ggc ctt cta taattcaaaa agcagagcca accagctctg cttttcttca	1068
Val Gly Leu Leu	
170	
ttttataga cgattaccga caccaacaag ggcacggta catatgttgt taaagactaa	1128
agtcaaatat ccctataaaa aggagctgaa atccatgagc tgcggaaaac accatggccg	1188
gcatgaaaat tgtgtatgcg atgcagtaga acagattata aaagaacagg atg	1241

<210> 16
<211> 170
<212> PRT
<213> *Bacillus licheniformis*
<400> 16

Met Glu Thr Arg Pro Tyr Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu
1 5 10 15

10295.204.ST25.txt

His Pro Gly Asn Asp Tyr His Pro Ser Tyr Pro Lys Lys Lys Leu Cys
 20 25 30

Asp Asp Tyr Thr Cys Asn Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile
 35 40 45

Asp Ser Asp Leu Asp Gln Leu His Leu Asn Lys Gln Leu Ser Asp Glu
 50 55 60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp
 65 70 75 80

Thr Gln Thr Leu Ala Ser Val Met Thr Ala Ala Gln Thr Leu Ala Val
 85 90 95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val
 100 105 110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln
 115 120 125

Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp
 130 135 140

Thr Asp Thr Ala Ile Ile Val Ser Thr Phe Val Gln Thr Val Val Ile
 145 150 155 160

Thr Ile Thr Ala Leu Ile Val Gly Leu Leu
 165 170

<210> 17
 <211> 1516
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1013)

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ggccgggcca	attccccggga	ggttttccag	gtgcggcgcc	atatggacag	atgccgaaaa		120
tgggagctcc	gtacggtatg	gggggatacg	gacagcagcc	tgcaggggga	cagatgttta		180
acagaccgga	agatgtatgaa	gactgattcg	aatgggacg	atgatctatc	gttccttttt		240
tatttgtggac	cgctataaaac	attttcatgc	tatttaacgg	aatgtctat	aactgtcaag		300
ggtaactctt	cgcatacccgc	acatcctaaa	aaagagcgca	atgctcaaat	tcagcggttt		360
tcacgggggg	tactaccatt	ggacagcaag	ctgaaaagtgt	tttcggggat	tttgcttttg		420
acagcaggtc	tatctgcatg	cggaacgaac	gacgctatacg	ataatggaaa	caatacgcgc		480
ccgatcggat	attatctcaa	atg atg cag atc	gtatc cag ggt	ctt gat aat			533

10295.204.ST25.txt

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn
 1 5 10

gac ggc cct gtt aca gaa atg ctt gaa aac atg aac ggg aga cac ggt Asp Gly Pro Val Thr Glu Met Leu Glu Asn Met Asn Gly Arg His Gly 15 20 25	581
gca aca aac gta aac aat cga gcg gga aac ggc aat ccc gtt cca aca Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr 30 35 40	629
ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu 45 50 55	677
gtg aat acg gcg gat aca ggc tat gac aga ccg gaa aac cgt aaa atc Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile 60 65 70 75	725
tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu 80 85 90	773
agc cag gca gtc gta acg aat gaa acg gtc atc atc gcc gta cgg tct Ser Gln Ala Val Val Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser 95 100 105	821
gat aaa agg ctg aca aat aac gag aga actcaa att aga aaa gca gcc Asp Lys Arg Leu Thr Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala 110 115 120	869
aaa aca ttt gcc gga gac cgg acc gtt caa gtt gtc gag gac gac ggc Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly 125 130 135	917
gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg 140 145 150 155	965
gat cgc gga gac acg acg aat aac aat ttg aac cgc ttg cgg aac caa Asp Arg Gly Asp Thr Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln 160 165 170	1013
taacaaggcag ggaattgccg gggattcccc ggcaattttt tataagcgct cggccgattc ctttacaaaa acggggaaaa ccgtataaag tgtacataga gacgagaatt attttgagg tagaaagtta tggctggcca ttctaaatgg aaaaatattc agagacgaaa aaatgccc gatgctaaac gcggcaaaat tttcatgaag cttgccaaag aaatatatgt agccgc gaagggggac cagatcccga atctaacgca agtctgcgtc tcgtcatcga taaagcc aatgcaaaca tgccaaatga caacatcgac cgccatca aaaaagcttc cggcagcc gatggaaaaa gctatgagga aattacgtat gagggctacg gaccaagcgg tggctgtc atggtaaat gttgacaga taataaaaac cggacggcga caagcgtcag aaccgc agcaaaaacg gcggcagctt ggg	1073 1133 1193 1253 1313 1373 1433 1493 1516

<210> 18
<211> 171
<212> PRT
<213> Bacillus licheniformis

<400> 18

10295.204.ST25.txt

Met Met Gln Ile Val Met Gln Gly Leu Asp Asn Asp Gly Pro Val Thr
 1 5 10 15

Glu Met Leu Glu Asn Met Asn Gly Arg His Gly Ala Thr Asn Val Asn
 20 25 30

Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr Gly Asp Gly Thr Tyr
 35 40 45

Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp
 50 55 60

Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr
 65 70 75 80

Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu Ser Gln Ala Val Val
 85 90 95

Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr
 100 105 110

Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly
 115 120 125

Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly Ala Phe Thr Arg Leu
 130 135 140

Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg Asp Arg Gly Asp Thr
 145 150 155 160

Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
 165 170

<210> 19
 <211> 1249
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (501)..(746)

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 atcaatttggaa accgtttttt gcattttggg gaatatcggt ttttctatcg caaatggctg
 gattgttttt atgctttcga tgtttggctc gacaatcgcc gaaattttat gttttcccttc 120
 aatgaatgtc cttttggacg agctggctcc ggatcatatg aaggcgccgt attacggcat
 gcaaaaactta tacaacatcg gtgagttttt agggccttgg ctggggggaa tgatgcttgc 180
 cttgtacggg ggaaaagccg tctttcttat tgctgcgtgt tcagtctttt tggcttttagg 240
 300
 360

10295.204.ST25.txt

cgcttaccat gtgggaagga gaaagttttt atctgcacag cattatggtg tatcgccctt	420
ttcttattga aaatttaggc cgcttatgca tgaatcatta agaattaccc aacctaaaag	480
gtaaaaaagg agtatgaatc atg gac aca aca ttg ggc tac ctc cgt gag tca Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser	533
1 5 10	
ctg tcg aat cac ctt gaa cac ggc ata gga caa aac att tac aga aaa Leu Ser Asn His Leu Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys	581
15 20 25	
atc gtt tcc ggg cga tat gcc aat gag gaa gag ttt gtc gag cac ttg Ile Val Ser Gly Arg Tyr Ala Asn Glu Glu Phe Val Glu His Leu	629
30 35 40	
gag gag cgg gaa atg gaa ttt ctg aat caa gtg ctt gaa cat gag atg Glu Glu Arg Glu Met Glu Phe Leu Asn Gln Val Leu Glu His Glu Met	677
45 50 55	
aaa tat gcg ctg aat gaa cag gac cat aaa cgg aca aga gaa tta aac Lys Tyr Ala Leu Asn Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn	725
60 65 70 75	
gaa gtg tat gaa ctg ctg ttt tgaaaggcgg gaatgatcaa tgggtgcaat Glu Val Tyr Glu Leu Leu Phe	776
80	
agagcggAAC ggatacacgt ttgaaccgga atacagcgt accagacaaa acgggtgcgt ccatgtatac cggcgccggcc gggttgcga ggagattccc tttgagtttc acggggagtt	836
tccagagcat gatttaattg aagagcttgt caatcattat tgttatgaaa ataaaatata	896
aggcttgaag aggctgccga ccgggcggct tttatTTTg gatTTTata tctataatcc	956
gcttgcagtt ttttagaacg gcagcagaaa agctgccata aatatgacag ctcatgcattc	1016
gctatTTTt ctttcgtcg tagtattgaa cagggatcat ggatcTTCC gataccattt	1076
tgttatCTTC gatatcatgc ggagacgggt gtcctgcttt ttcaaccggg aatgaatcta	1136
cgttgtttt ttccgaaaag taagggatct tttctttgac gttttgcaag tac	1196
	1249

<210> 20

<211> 82

<212> PRT

<213> Bacillus licheniformis

<400> 20

Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser Leu Ser Asn His Leu	
1 5 10 15	

Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys Ile Val Ser Gly Arg	
20 25 30	

Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu Glu Glu Arg Glu Met	
35 40 45	

Glu Phe Leu Asn Gln Val Leu Glu His Glu Met Lys Tyr Ala Leu Asn	
50 55 60	

10295.204.ST25.txt
Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn Glu Val Tyr Glu Leu
65 70 75 80

Leu Phe

<210> 21
<211> 1620
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1121)

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 Asp Glu Ala Val Gln Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp
 15 20 25

gat gtc gaa gtc gac gta gtt gat gaa gga aaa aag gga tta ttc ggc
 Asp Val Glu Val Asp Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly
 30 35 40

att ttc ggt cat cg^g tct gca gtc gt^g aac att cg^g gaa aaa ata gac
 Ile Phe Gly His Arg Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp
 45 50 55 677

ccg gtt aaa gaa gca aaa caa tat ttg gaa aat gta att tcg aat atg
 Pro Val Lys Glu Ala Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met
 60 65 70 75

gga ata caa gcc cag gtg acg gca gaa gag gag tct aaa cga gtg gtt 773
Gly Ile Gln Ala Gln Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val
80 85 90

ttt cag ttg aaa gga gac aaa aca gct ctt tta att gga aaa agg gga
Phe Gln Leu Lys Gly Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly
95 100 105 821

caa act tta aat gcc ctt gaa acg ctg acg cag ctc gtg ctc aat cgt
 Gln Thr Leu Asn Ala Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg
 110 115 120

cat tcc gac aga tat atc caa gcg gtg gtt gac gcc gaa gga tac cgc 91

10295.204.ST25.txt

His Ser Asp Arg Tyr Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg			
125	130	135	
gca aag cgg aag gaa aca ctt gct cag ctg gca ttg aag ctt gct gac			965
Ala Lys Arg Lys Glu Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp			
140	145	150	155
cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc			1013
Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser			
160	165	170	
agt gag cgc aag gtc atc cat gat acg ctt gcg ggc tac tcg cag cat			1061
Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His			
175	180	185	
atc gaa act tac tct acc ggt gaa gac cat aac ccg cac ctt gtc atc			1109
Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile			
190	195	200	
tca tat aaa aaa taacatgaaa accgaagttc ccaaaattgg ggcttcgggtt			1161
Ser Tyr Lys Lys			
205			
ttttgccgt tgaaaatcga tgaaaatgcag caaaaatcagt ttaagttcta ttttttcagg			1221
cgtaagctgt tgatgaaaat gaaatttaat tggttattcac atgtggataa gttaaagtaa			1281
gtaatgatgg cttagaacgg ttgtggataa cggttcaagt cacttccact tcaattgaaa			1341
ctatgttatac tttaaatttt gattacaata aaagttttc atccgtatac gatgtttgga			1401
agatgacccg gcaaattggg ataatagata taggaatgaa aaagagaggt gaaagccatg			1461
gataccatcg ctgcgatttc aacgcccgt ggagaagggg cgattgcgt cgtccggatg			1521
agcggccctg aggctttgc gatgccgt aaagtgtata aaggacctcg cgaaaaagg			1581
ctgagttccg tcgattcaca tacgattaac tacggcat			1620

<210> 22

<211> 207

<212> PRT

<213> *Bacillus licheniformis*

<400> 22

Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val Asp Glu Ala Val Gln			
1	5	10	15

Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp Asp Val Glu Val Asp			
20	25	30	

Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly Ile Phe Gly His Arg			
35	40	45	

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala			
50	55	60	

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln			
65	70	75	80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly	
Page 25	

85

10295.204.ST25.txt

90

95

Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly Gln Thr Leu Asn Ala
 100 105 110

Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg His Ser Asp Arg Tyr
 115 120 125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu
 130 135 140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln
 145 150 155 160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val
 165 170 175

Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His Ile Glu Thr Tyr Ser
 180 185 190

Thr Gly Glu Asp His Asn Arg His Leu Val Ile Ser Tyr Lys Lys
 195 200 205

<210> 23
<211> 1614
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1115)

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gccaaaaacg tatccgctcc attttgcgt aaatccgtcc gaatagctgc caagcgtctc 120
aatatacagg gaaagaaaacg gcagaaccat tgtggagctt gcggccacga aaaaattcgc 180
aaaccacatg atcacaaggt ttttcttata aacagagatg cgaatcacct tcttaaaaaa 240
tttgaattcc ctttcattat aaatgaaatg cgaaagctgc atgaaattga tgctctatag 300
aatgacgaaa aatgggcatt tgaaggaatt ttcaacattt tcagaaaata aaaccttaaa 360
tatagaaaata taatgatata ataagagaaa tatgagcgta ctttgaaaaa cattcagaag 420
actataggct tggataattt caatccgctg cgttaccacc ataagtttt tatattgaga 480
tagaaaggca ggtgtgaaag ttg gaa gcg agc acc tta ctg att att gat ttt 533
Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe
1 5 10

gaa ttt aca atg cct gag gga aag tat cac ccg caa aat ttt ttc ccg 581
Glu Phe Thr Met Pro Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro
15 20 25

gaa atc ata gaa gca ggg att gta aag acg gtt cat gat gag gtc gtt 629
Glu Ile Ile Glu Ala Gly Ile Val Lys Thr Val His Asp Glu Val Val

10295.204.ST25.txt

30	35	40	
gag acg ttt tca agc tat att aag ccg aag aag ttc cct aaa tta acg Glu Thr Phe Ser Ser Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr	45	50	677
agg cgc tgc aaa aat ttt ctc agc atc acg cag gaa cag gtt gac caa Arg Arg Cys Lys Asn Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln	60	65	725
ggc atc acg ttt aac gcg ctg att gaa aag ctg cgg gag ctt gat cct Gly Ile Thr Phe Asn Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro	80	85	773
gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gta Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val	95	100	821
ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly	110	115	869
gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys	125	130	917
aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly	140	145	965
acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys	160	165	1013
ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys	175	180	1061
ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His	190	195	1109
gcc aca taaaaaaccc aatctgacaa acagattggg ttatttgac agggaaatatt Ala Thr	205		1165
cttttcaag cccatgaata agctcaagcg attttgcgcgt gtattcggac gaatcgaaaa gcagatccgt ttttaagcgg ctcaaagctg agcggagcga atccgcataa tccggtagac cttcatcgaa cggttcacc atgcgggtcg ggatattcgt ctgttcaccg taagcgagcg cttttcgttc atgaaaaaaaaa gggacgtctg cccgattggg atgatgaagg tcgcccgt tcggatgggt cagcacggcg aggatttga ccaggttagtg catcggttta acatccgtaa tttcggatgttgcgttataaaa agccctttac gcgatctccg acttgaaatt ggtgttcac tgcatctgccc tcctaattgtt atcataataa ataaaatggta aaaaaatcat ttcaggagg aagaaaaatg gcgcgttt			1225 1285 1345 1405 1465 1525 1585 1614

<210> 24
<211> 205
<212> PRT
<213> *Bacillus licheniformis*

10295.204.ST25.txt

<400> 24

Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe Glu Phe Thr Met Pro
1 5 10 15

Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro Glu Ile Ile Glu Ala
20 25 30

Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser
35 40 45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn
50 55 60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn
65 70 75 80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val
85 90 95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys
100 105 110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu
115 120 125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu
130 135 140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His
145 150 155 160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val
165 170 175

Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys Pro Thr Thr Ile Gly
180 185 190

Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr
195 200 205

<210> 25
<211> 1600

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1097)

<400> 25

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tgttcatttt gaagtgtttt ggcaaagcct tcagcgaatt ttggatcttc aaagacttt 120

10295.204.ST25.txt

ttccaaaatt cagtccttt tttggaggc attgtttttt caacggtttca ttgacagtt	180
tttcatcca ttacaagtgt ttcatttaat ttgtcatcat ttaatatttc ttgaatcgct	240
tttttccgt catctgtctt taatatatcg acaaccattt tttggtttg atcatagtc	300
atctcagctg cttggccgt gggagcacaa gctgttacag atagaaacag aaaacagctt	360
atcgatagca ttgcggtctt gaacatgctt aagctccctt cgaaaactcg tcttaccctt	420
aatatgaatg tctttaaaaa atttatacat aacaaaatat cgctgttaca gcggtttatt	480
taggggttgg gaagtctaca atg aaa agc cgt aat ctc gtc cga ttt ttc ttt Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe	533
1 5 10	
tcc gta ttg ggt gtc gga gct ttg act aca agt att gtc ggt ttt gcc Ser Val Leu Gly Val Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala	581
15 20 25	
ata gag tgg gga aga tat aag gag ctg ttt ctt tcc ttc gag gta ttg Ile Glu Trp Gly Arg Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu	629
30 35 40	
gag att ctg tct gtt ctt ttc tgg ttt atc ggg gtt ggc atg atc ttt Glu Ile Leu Ser Val Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe	677
45 50 55	
agc gtg att gct caa atg gga ttt gtg att ttc tta acg att cac cgc Ser Val Ile Ala Gln Met Gly Phe Val Ile Phe Leu Thr Ile His Arg	725
60 65 70 75	
ttt gca ctg gaa att ttc aga tct cat tct ttg tgg aat tcg att cag Phe Ala Leu Glu Ile Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln	773
80 85 90	
ctg ttt ttg att ata ttt gtc gcg ttt gac ttg gtt tac ttg cgc ttt Leu Phe Leu Ile Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe	821
95 100 105	
ctg ttt ttg gaa aaa gat gga ggc tcc atc att ccg tac att ttg ctg Leu Phe Glu Lys Asp Gly Ser Ile Ile Pro Tyr Ile Trp Leu	869
110 115 120	
ccg ctc ttt att ttg gcg gta ggc att gcg gcc gct tat gca aag caa Pro Leu Phe Ile Leu Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln	917
125 130 135	
aaa cag tcc tct aaa aaa acg ttc gtt tcc gca tta ttt cta atg ttt Lys Gln Ser Ser Lys Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe	965
140 145 150 155	
gtt ttt act gtg atg gag tgg ttc ccg gcg tta agg gtc aat gaa gag Val Phe Thr Val Met Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu	1013
160 165 170	
gac tgg ctc tat tta atg ctg ctt cct tta tta gcc tgc aac gct ttt Asp Trp Leu Tyr Leu Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe	1061
175 180 185	
cag ctt tta atg ctg cca aaa ttt cag gca cgc gct tagaccggct Gln Leu Leu Met Leu Pro Lys Phe Gln Ala Arg Ala	1107
190 195	
gctactttac ttctgaagat tttgcattcg tatttgcgt taattcgctg actgttacgt	1167
ttttgagccc cttgcttctg agatggtgca cgatctctgg cagggcttct tttgtttgtt	1227

10295.204.ST25.txt

tggcggaaatc tgaagcgtga aagagcacga tgcaccggc gtttaccgtt ccatttacgt	1287
tttggacgat ctttgaacc cccgggttcg tccagtcatc cgagttataa ctataatgaa	1347
caacgggtgt aacgtactgt ttagcaacat cgagtacgtc tttattaaac tggccggtcg	1407
gcggcttaa aagcgtaagg tcgtcaagcc cgagttttg aaaggagtgt cgtgctttg	1467
ctaagtcttt tttgatctcg cttttcttca ttgcgaata gttttataa gcatagccca	1527
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ccccatgaagc tga	1600

<210> 26

<211> 199

<212> PRT

<213> *Bacillus licheniformis*

<400> 26

Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe Ser Val Leu Gly Val			
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Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala Ile Glu Trp Gly Arg			
20	25	30	

Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu Glu Ile Leu Ser Val			
35	40	45	

Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe Ser Val Ile Ala Gln			
50	55	60	

Met Gly Phe Val Ile Phe Leu Thr Ile His Arg Phe Ala Leu Glu Ile			
65	70	75	80

Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln Leu Phe Leu Ile Ile			
85	90	95	

Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe Leu Phe Phe Glu Lys			
100	105	110	

Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu Pro Leu Phe Ile Leu			
115	120	125	

Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln Lys Gln Ser Ser Lys			
130	135	140	

Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe Val Phe Thr Val Met			
145	150	155	160

Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu Asp Trp Leu Tyr Leu			
165	170	175	

Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe Gln Leu Leu Met Leu	
Page 30	

180

10295.204.ST25.txt

185

190

Pro Lys Phe Gln Ala Arg Ala
195

<210> 27
<211> 1991
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (489)..(1499)

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gaagtggccg acatcaacgg cctgactgca caggaagtca tcgatattca cacctcggt	240
gagtagctcg tttatatgat cggcttgcg ccgggcttcc cttacctagg cggaatgtct	300
gaaaagatag ccgcaccgcg gcggtcatct cctcggaactt cgattcccgc cggttcagtc	360
ggaatagccg gcatgcaaac aggcgtctat cccctttcaa cgccgggcgg ctggcagctg	420
atcggcaata cgccgcttga attattcaag ccttatgaac agcctccgag ccttctgaga	480
gcaggggata tcgtgaaatt tgtcagcgtg acagaagagg agtatcacgc gctgaaggag	530
gggaaatc ttg agc ata gaa gtg tta aag ccg ggt ctg atg aca acg gtt	578
Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val	
1 5 10	
caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc	626
Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser	
15 20 25 30	
ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg	674
Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly	
35 40 45	
aac agc cag aac gaa gct gcg ctt gaa gtg acg ctg atg ggg ccg ggg	722
Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly	
50 55 60	
ccg tct ctc cgc ttt caa aaa cct gct ctt ata gcg gtg acg ggc gct	770
Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala	
65 70 75	
gac ttt tca ctg atg gta aat gac gaa gaa gtc ccg ctt tgg cgc ccg	818
Asp Phe Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro	
80 85 90	
gtt ttc atc aaa gag ggc agc gtg ttg aca ttc ggc atg tgc aag cgc	866
Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg	
95 100 105 110	
gga agc cgt gca tat atg gca gtg gcc ggg gga att gat gtg ccg cct	914
Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro	
115 120 125	
gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt	
Val Met Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Phe	

10295.204.ST25.txt

130	135	140	
caa gga agg gcg ctt caa aag gga gac gtg tta tcg cta ggc agc ccg Gln Gly Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro 145	150	155	962
acg ccg ttg tcg gaa gcg ctg cac aga aag ctc gca gac gag ggc aaa Thr Pro Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys 160	165	170	1010
gaa cg ^g ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe 175	180	185	1058
ctc ccg cta aaa aag aac ccg gtc att cgt gtc atc aaa ggc gat cag Leu Pro Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln 195	200	205	1106
ttt gct tgc ttt acc tca tca tca caa gag cgc ttt ttc gcg ggt cca Phe Ala Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro 210	215	220	1154
ttc ccg gtg acg gct aaa tcc gac ccg atg ggg tac cgt ctt caa gga Phe Arg Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly 225	230	235	1202
gag gcg ctc gaa ctc act cag cct ctg gaa atg atc tct gaa gcg gta Glu Ala Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val 240	245	250	1250
tca ttc gga acg att caa gtg ccg ccc gac ggc aat ccg atc gtt ctt Ser Phe Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu 255	260	265	1298
ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile 275	280	285	1346
gca tca gct gat ttt tct cag gtc acg cag atg atg ccg ggc gag cag Ala Ser Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln 290	295	300	1394
gtg cag ttt cag ctt gtc agc ctt cag gaa gca gag cgc gtt tac atc Val Gln Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile 305	310	315	1442
gaa ccg gag acg aaa atc agc gaa ctt tct gcc cga ttg aag ctt gaa Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu 320	325	330	1490
tac atg tta tgataggtgt gatgtgtatc aggaggggga aggcatggaa Tyr Met Leu 335			1539
cataaaaaaca aaacagtgcgt caaaggccatg accctgctca atctgttcct gacgagagaa			1599
aggctctcgc tggcgacat gattgagctg acaggcatgc cgaaaacatc tgtctaccgc			1659
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tttaggactgc tgaaaaatgc atacggccac cttgtttcag aaaggcttga tattcgaaaa			1779
atcgctctgc ccatcatgga agaactccgc gatgacgtgg atgaagccgt ccatttaatt			1839
gtaaggcagg gaaatgaagc aatgtatata gaaaaaattt agggcacgca gaccgttcgc			1899
ctctatacag cgatcggag gcggccccct ttatatgccg gagcctgtgc gagaagcatt			1959

10295.204.ST25.txt

ctgacgtttt tgccctgaaga ggagcggat gc

1991

<210> 28
<211> 337
<212> PRT
<213> *Bacillus licheniformis*

<400> 28

Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val Gln Asp
1 5 10 15

Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser Gly Ala
20 25 30

Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly Asn Ser
35 40 45

Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser
50 55 60

Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala Asp Phe
65 70 75 80

Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe
85 90 95

Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser
100 105 110

Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met
115 120 125

Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe Gln Gly
130 135 140

Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro Thr Pro
145 150 155 160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg
165 170 175

Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe Leu Pro
180 185 190

Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala
195 200 205

Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg
210 215 220

Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala
225 230 235 240

10295.204.ST25.txt

Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val Ser Phe
245 250 255

Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu Leu Ala
260 265 270

Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile Ala Ser
275 280 285

Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln
290 295 300

Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile Glu Arg
305 310 315 320

Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu Tyr Met
325 330 335

Leu

<210> 29
<211> 2287
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1784)

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tatgagctgc ttacatttaa ctggatggcc cattcgctga cgcttgaata tgaggtgatc	240
ggtcaagtca aggatttgtc agcttatgaa gaaaggctcg tcgttctcat cagaaagctg	300
tttgggattt ttgacgatgc cgaaaaaa ggcagcgaca atcatctgac gatcacgctg	360
cagacggacg gtccggacga ccgcctcgatcttctcg atttccacgg cgtattcaca	420
aagctgaccg gtatcaaaga ctttcatcat tcactggccg acttttatga aatcaagcgg	480
tttcatgtaa cagaccgtga gtgcattcgcc gaaattcata tcaagtaaag cggttttta	533
ggaatagaac ggaggacatt atg ttt gtt gat cag gtg aaa ata tac gta aaa	581
Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys	
1 5 10	
ggc gga gac gga ggc aac ggt atg gtt gct ttc cgc cgc gaa aaa tat	629
Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr	
15 20 25	
gtg cca aaa gga ggc cct gcc gga ggt gac ggc gga aaa ggc gga gac	
Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp	
30 35 40	

10295.204.ST25.txt

gtc gtt ttc aaa gtt gac gaa ggt ctc agc acg ctg atg gat ttt aga Val Val Phe Lys Val Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg 45 50 55	677
tat caa aga cat ttt aag gca gcg cgc gga gaa cac ggc atg tct aaa Tyr Gln Arg His Phe Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys 60 65 70 75	725
aac cag cac ggc cga aat gcc gaa gac atg gtt gtg aaa gtc ccg ccc Asn Gln His Gly Arg Asn Ala Glu Asp Met Val Val Lys Val Pro Pro 80 85 90	773
ggc acg gtt gtc att gac gat gat aca aaa cag gtc atc gct gat tta Gly Thr Val Val Ile Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu 95 100 105	821
acg gag cac gga cag gaa gcc gtc atc gca aaa ggg gga cgc ggc gga Thr Glu His Gly Gln Glu Ala Val Ile Ala Lys Gly Arg Gly Gly 110 115 120	869
cgg ggc aat aca cgt ttt gcg acg cct gcc aac ccg gcg ccg cag ctt Arg Gly Asn Thr Arg Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu 125 130 135	917
tct gaa aac ggc gaa ccc ggc aag gag cgc tat att gtt ctc gag ctg Ser Glu Asn Gly Glu Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu 140 145 150 155	965
aaa gtt ttg gca gat gtc ggt ctt gtc ggc ttc cca agc gtc gga aaa Lys Val Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys 160 165 170	1013
tca acg ctc ctg tct gtc gtg tct tcg gcc aag ccg aaa att gcc gat Ser Thr Leu Leu Ser Val Val Ser Ala Lys Pro Lys Ile Ala Asp 175 180 185	1061
tac cac ttt aca acg ctg aac ccg aat ctc gga atg gtc gaa acg gaa Tyr His Phe Thr Thr Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu 190 195 200	1109
gac ggc cgc agc ttt gta atg gcg gat ctt ccg gga ctg att gag ggg Asp Gly Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly 205 210 215	1157
gcg cac gaa gga gtt ggc ctc gga cac caa ttc ctc agg cat atc gaa Ala His Glu Gly Val Gly Leu Gly His Gln Phe Leu Arg His Ile Glu 220 225 230 235	1205
aga acg cgc gtc atc gtg cac gtt att gac atg tcg ggt ctt gaa ggg Arg Thr Arg Val Ile Val His Val Ile Asp Met Ser Gly Leu Glu Gly 240 245 250	1253
cgc gac ccg tat gaa gat tat gtg acc att aat aaa gag ctt gaa cag Arg Asp Pro Tyr Glu Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln 255 260 265	1301
tat aat ctc agg ctg aca gaa cgt cct caa att att gtc gcc aat aaa Tyr Asn Leu Arg Leu Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys 270 275 280	1349
atg gat atg ccg gat gcg gaa gaa aat ctg aag gct ttc aaa gaa aag Met Asp Met Pro Asp Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys 285 290 295	1397
ctc aca gat gat tat cct gtt ttt cca atc agc gcg gtg acc aga caa Leu Thr Asp Asp Tyr Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln 300 305 310 315	1445

10295.204.ST25.txt

ggc ttg agg gat ctg ctg ttt gaa att gcc gac cgt ttg gaa acg acg Gly Leu Arg Asp Leu Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr 320 325 330	1493
ccg gaa ttc ccg ctc tac gac gaa gaa gac atg gct gaa aac aga gtc Pro Glu Phe Pro Leu Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val 335 340 345	1541
atg tat aag ctt gag gat gag gaa gcg ccg ttt gag atc agc cgt gat Met Tyr Lys Leu Glu Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp 350 355 360	1589
cct gac ggc acc ttc gtg ctc agc gga gcc aag ctt gaa cgc tta ttt Pro Asp Gly Thr Phe Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe 365 370 375	1637
aaa atg acg gac ttt tca aga gat gag tct gtt aag cgt ttt gcc aga Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg 380 385 390 395	1685
cag ctt cgcc gga atg ggc gtc gat gat gcg ctt cgcc ggc cgc ggt gca Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala 400 405 410	1733
aaa gac ggg gat acg atc cgt ctt ctc gaa ttt gaa ttt gaa ttt atc Lys Asp Gly Asp Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile 415 420 425	1781
gac tgatcatacc ggagagtttgc caaaggcaagc tctccgactt ttagctgaaa Asp	1834
ggaacgccct tccttcgca gcatcaatgt aaaggaatca gggtttttaa aaggagagaa aagtctgtga aagaggagac cttttatctt gtcaggaaag acgtgctgcc ggaggcaatg cgaaaaacac ttgaggtcaa aaagctgatt gagcggaaaa aagcggaaatc tgttagctgaa gccgtacaaa agtagattt gagccaaagc gcttttata agtacagaga tgcggtttt ccttttata ccatggtcaa ggaacagatt atcacgctt ttttcattt ggaggaccgc tcaggaacgc tgcggatct gctgcaagtg gtagctgaat cgggctgcaa tgcgtgtcg atccaccaga ccatccctct tcaaggaaga gcgaatgtca cgctctctgt cagtacgaga ggcatggatg aaaatatcga tttgctgatg aac	1894 1954 2014 2074 2134 2194 2254 2287

<210> 30
<211> 428
<212> PRT
<213> *Bacillus licheniformis*
<400> 30

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
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Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Asp Val Val Phe Lys Val
35 40 45

10295.204.ST25.txt

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
50 55 60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65 70 75 80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
85 90 95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
100 105 110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Arg Gly Asn Thr Arg
115 120 125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
130 135 140

Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp
145 150 155 160

Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser
165 170 175

Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr
180 185 190

Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe
195 200 205

Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val
210 215 220

Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile
225 230 235 240

Val His Val Ile Asp Met Ser Gly Leu Glu Gly Arg Asp Pro Tyr Glu
245 250 255

Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln Tyr Asn Leu Arg Leu
260 265 270

Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys Met Asp Met Pro Asp
275 280 285

Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys Leu Thr Asp Asp Tyr
290 295 300

Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln Gly Leu Arg Asp Leu
305 310 315 320

10295.204.ST25.txt

Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr Pro Glu Phe Pro Leu
 325 330 335

Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val Met Tyr Lys Leu Glu
 340 345 350

Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp Pro Asp Gly Thr Phe
 355 360 365

Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe
 370 375 380

Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg Gln Leu Arg Gly Met
 385 390 395 400

Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala Lys Asp Gly Asp Thr
 405 410 415

Ile Arg Leu Leu Glu Phe Glu Phe Ile Asp
 420 425

<210> 31
<211> 2115
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1616)

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gttccagcgt ttgatctatt gcatttgca gcccgtgaac atcaagagtc ttcatggcat	240
tctcctctaa tcctttcat tacaatcagt atatagttt ccactttata gaaagtactt	300
ggtaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatattctat	360
tgattcattt cgattaccgt aaacaagttt gtttagcat tctttaggct ctgtgactaa	420
acccaaaaagc catttggttt aaattggctt ttcggtatca cgaaaatttc gttttttggg	480
ctgatagaag ttttgcattt atgaatttgcata tgttaatctt taacataaaa aggatgttag	533
ctggaaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc	581
Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile	
1 5 10	

aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa	581
Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu	
15 20 25	

gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa	629
Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu	
30 35 40	

10295.204.ST25.txt

gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His 45 50 55	677
gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys 60 65 70 75	725
tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly 80 85 90	773
ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct Leu Leu Glu Tyr Tyr Phe Ser Phe Thr Gly Met Tyr His Phe Ser 95 100 105	821
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys 110 115 120	869
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr 125 130 135	917
aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met 140 145 150 155	965
tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr 160 165 170	1013
gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile 175 180 185	1061
gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Ser Ala Lys 190 195 200	1109
gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu 205 210 215	1157
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala 220 225 230 235	1205
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala 240 245 250	1253
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg 255 260 265	1301
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu 270 275 280	1349
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val 285 290 295	1397
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu 300 305 310 315	1445

10295.204.ST25.txt
aca atg aaa cca tta cg^g gat agt cgt ggt tac ccc tat ctt gag gaa 1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu
320 325 330
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cg^g cca aat 1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn
335 340 345
gat tcc ata ttt ttt tat gat cag atg gt^g cag gct cag aaa caa atc 1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
350 355 360
aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga 1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile
365 370
cccttgcttt gggcttggtt gtcgtgtcga gcgc^tttccat tcacacatct gttgaacaac 1696
aacatgcaga attttctgtta gcatcttaggc tcgcaacata attgtgttt ggcagg^tcat 1756
gtgatggcct gccttttgg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816
taatactcat ctttcttcgt cccttg^tgtt ggaattttca tcata^tcaat atttgaatat 1876
gcggctgtcc gcattattaa caatttaaa tttttgcac aaattttata caaaggcaga 1936
caaaaacctt gatatatcaa tgg^ttctatg ggtatattca accacgacca ccgatatcgc 1996
taaaaaccgt attgccaaac gacgaaagag cgttc^tttac acaaggaatg ctcttttgt 2056
ttattcctca tcaaagcgga gagccgcca^a cataaacgca atgaccaact gttgtccgc 2115

<210> 32
<211> 372
<212> PRT
<213> *Bacillus licheniformis*

<400> 32

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
1 5 10 15

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
100 105 110

10295.204.ST25.txt

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
145 150 155 160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
355 360 365

Leu Tyr Glu Ile
370

10295.204.ST25.txt

<210> 33
<211> 2077
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1574)

<400> 33	ttgattaaag tggaaatatt taaaaaaaaca tgtatggtaa taaaaaatct tttcgtaat	60	
	aatattatg gtcttttcc tactttaaca aggataatc ttccctcta ttgaatgtaa	120	
	tatagtaaag cgaatagagg agggatataca aatgaatcct tactatatga tgctttatg	180	
	ttatgtccta tcgatcatcc acttttaat aggctaccgg gaagccctga aaataagcgg	240	
	ggttgcggg ctggtaacg gaaccgcaat gatctcctgt attccgcttg gcgcgggttt	300	
	cgctttttc gcgcactttt ttggaaaat gacgatttaa ttccggaaat gaatttttc	360	
	gccaacaaac atgcatttcc gtgttattca cagacggcgg cagtttatgc tatgattaat	420	
	agaacttcaa ttacaaaaa attcacaaag attggggaa aaagaatggc caaagccggg	480	
	ttctcaaga agtcgccaat atg ctg aac gac tgg tac ata ctg atg aaa aaa	533	
	Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys		
1	5	10	
cga gac att tca ggt tca atc gaa atg aaa gat gac ata gat aaa gca	581		
Arg Asp Ile Ser Gly Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala			
15	20	25	
att gaa aag atg gaa gaa gat cat gac gtt ctt ctc tat tat caa atg	629		
Ile Glu Lys Met Glu Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met			
30	35	40	
ctg gat ttt cgc tta agg ctt ctt gaa gat atc tcc caa tct tcc	677		
Leu Asp Phe Arg Leu Arg Leu Leu Glu Asp Ile Ser Gln Ser Ser			
45	50	55	
aca gaa aaa ttg gaa gcc atc agt ttt aag gac aaa gat cca aaa agt	725		
Thr Glu Lys Leu Glu Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser			
60	65	70	75
acg gac gat aag ctg aat tat tat ttt tat ctg ttc aaa ggg att tat	773		
Thr Asp Asp Lys Leu Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr			
80	85	90	
gaa gac tac aag caa aac cat aca gaa gcg ctt aat ttt ttc aga ata	821		
Glu Asp Tyr Lys Gln Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile			
95	100	105	
gcg gaa aaa agg ctg agc gtc att caa aat gaa att gaa aaa gcc gaa	869		
Ala Glu Lys Arg Leu Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu			
110	115	120	
ttt cat tat aaa atc ggt gtt ttg tat tac aac tta aaa gcg aca tgg	917		
Phe His Tyr Lys Ile Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp			
125	130	135	
ctg tcg att cac cac atc aac att gcc tca ggc atc ttc caa ggg tat	965		
Leu Ser Ile His His Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr			
140	145	150	155
gac ggg tat gcc aag cggtc atc aac tgc aaa atg ctg atc ggg ctc	1013		

10295.204.ST25.txt

Asp Gly Tyr Ala Lys Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu
 160 165 170

aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag 1061
 Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys
 175 180 185

gaa gca att gaa aaa acc gaa aaa atc ggc gac caa tat ctt ttg cct 1109
 Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro
 190 195 200

tat acc tac tat aat atg ggc ttt ttg aag agt aag gaa gat aaa cac 1157
 Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His
 205 210 215

gaa gaa gcg ctg aag tat tat aat aaa gct ttt gca atc aaa gac ttt 1205
 Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe
 220 225 230 235

gaa acg aaa gcc aag tat gct tac ctt cta tgt gta tat gaa aac aca 1253
 Glu Thr Lys Ala Lys Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr
 240 245 250

agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc 1301
 Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile
 255 260 265

gac aca ggc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa 1349
 Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu
 270 275 280

tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa 1397
 Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys
 285 290 295

ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca 1445
 Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala
 300 305 310 315

tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg 1493
 Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg
 320 325 330

gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac 1541
 Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp
 335 340 345

aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt 1594
 Lys Ala Ser Lys Leu Ala Gly Arg Gly Glu
 350 355

tagctgtatt tggatttaggc actgtttca gctttcggt tgcaaatcac gctccgtgaag 1654

cggctcccc aagcaatgag atactttgg cttctcggtt agcaggcggt tgactacatc 1714

ctcaaaatac ccattcagac atctgctgaa tgggtatccc gcactttaca ttcatattca 1774

ggagtgatcg atatggaaa gaaagtactg ctgacaggat ttgaccctt tgggggagaa 1834

acagtcaatc cgtcctggga agcttaaaa cggctgaacg gagaggaagc agaaggcgtc 1894

tctatcgcat cggagcagat tccgaccgtt tttcatcatt cagcggccgt tttgaaaaaa 1954

gcgatcgaaa agcacaaacc cgatgtcgtc atttgcgcag ggcaagcagg cggcaggcgt 2014

catattacgc cggaacgcat cgcaatcaac atcgatgatg ctcgcattcc ggataatgaa 2074

gac 2077

10295.204.ST25.txt

<210> 34
<211> 358
<212> PRT
<213> *Bacillus licheniformis*

<400> 34

Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys Arg Asp Ile Ser Gly
1 5 10 15

ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala Ile Glu Lys Met Glu
20 25 30

Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met Leu Asp Phe Arg Leu
35 40 45

Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu
50 55 60

Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu
65 70 75 80

Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln
85 90 95

Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu
100 105 110

Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile
115 120 125

Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His
130 135 140

Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys
145 150 155 160

Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln
165 170 175

Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys
180 185 190

Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn
195 200 205

Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys
210 215 220

Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys
225 230 235 240

10295.204.ST25.txt

Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys
245 250 255

Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys
260 265 270

Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr
275 280 285

Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys
290 295 300

Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu
305 310 315 320

Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr
325 330 335

Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp Lys Ala Ser Lys Leu
340 345 350

Ala Gly Arg Gly Gly Glu
355

<210> 35
<211> 2101
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1598)

<400> 35	60
aaaacagcat gggctaaaat gacgctggac aaagcagtgt ccttaggctt ggaggcaaat	120
gcattttga aaagaaacac agacggaaaa gaactgagct gcagccggc tggagaaaaa	180
ggaaaagtgc tcccggggca gacatcctgt tatacaccga tggttgattt cgatccgcgt	240
tcttcatatg cgatgtagaa acattatcaa tccattaaca ggagctctca cttattccta	300
tacaagttcg tattcatatt tgaagaagta gtgtataaaa gcacccttgc agcaagggtg	360
cttttgctg tcttatcagt cacggttca cagctattga agagtcattt gacctaataa	420
aagagtggga aagtggggg attcaggaaa ctgtgtaaaa tgaactatta ctattaattt	480
atacaggggag gaaaatatac tatgatatga ataatgaata aaataaaaaa aaattgaata	533
tcggaagaaa ggagctccat atg aac aag atc gcc gcg gaa gaa gtc gcc aac	
Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn	
1 5 10	
atc ctt aat aca tgg tac cgc gcc atc aga aga aat gat gct gaa cag	581
Ile Leu Asn Thr Trp Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln	
15 20 25	

10295.204.ST25.txt

tcg atc cga ata ttt gaa gaa gtc aaa ccg atg ctg gca gag atg gag Ser Ile Arg Ile Phe Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu 30 35 40	629
gaa gac caa gag gtt tta atc tac tat tct ctg ctg gaa ctg cg ^g cat Glu Asp Gln Glu Val Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His 45 50 55	677
aaa atc atg ctg tat gat acg cg ^g gga aaa aag ata gaa cag caa gag Lys Ile Met Leu Tyr Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu 60 65 70 75	725
gag tta acg aac gg ^c ggc agt gct gca tca cat atg aca tcc tat tac Glu Leu Thr Asn Gly Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr 80 85 90	773
tac tac ctg ttt tca gga gct tat gaa gtg tat aaa aag aat tat gag Tyr Tyr Leu Phe Ser Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu 95 100 105	821
cag gcg atc agc ttc tat aaa att gcc gag aag aag ctt gct cat gta Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val 110 115 120	869
cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu 125 130 135	917
tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cg ^g cag Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln 140 145 150 155	965
g ^c g atg gaa att ttc aag ggg cat ggc gac cat gat atg aac ctt gtt Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val 160 165 170	1013
tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr 175 180 185	1061
aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys 190 195 200	1109
gcc ggc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu 205 210 215	1157
ctt tat g ^c g g ^c g atg gac aat tcg gaa aaa agc att cag ttt tta gaa Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu 220 225 230 235	1205
atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn 240 245 250	1253
gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys 255 260 265	1301
cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc g ^c g Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala 270 275 280	1349
g ^c g aat aaa ata ttt gac gcc aaa atc gat att tta tat g ^c g gct tat Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr 285 290 295	1397

10295.204.ST25.txt

gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu 300 305 310 315	1445
atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu 320 325 330	1493
tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala 335 340 345	1541
cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val 350 355 360	1589
gag gga atg tgatgaaaaa actgttcatt gttgctgcga ttgctgccgt Glu Gly Met 365	1638
cgtatgttcg ggatggtttg cgccagaac tcactggca tccggcgaca tgcagggtgc tgaaaagatg gtcggtaaa tcgaataactc ggaacaaata tgaacatccg ctcctgagca tcagggcga ttttttggg aaggtaaagt aaattaaggc ataagaaacg cggtagaca atgaacacctt ctaccactt attagggtg gtcaacctaa acaaaggta gaaacctgtg ctgactactt ttactccgat gtccttcag ctattctgt cagtaagatc attccccatc tcttcaacgc ctcaggcatc acctattaaa aaaatcataa ttgaaacttg tcagcaaata tgttgataa cacgaggatg tttccacaat aattaaacat taagactttt ttgacttcca gaaggaagaa caagatattt atgtaaaatc actcttttat tca	1698 1758 1818 1878 1938 1998 2058 2101

<210> 36
<211> 366
<212> PRT
<213> *Bacillus licheniformis*

<400> 36

Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp
1 5 10 15

Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe
20 25 30

Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val
35 40 45

Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr
50 55 60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly
65 70 75 80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser
85 90 95

10295.204.ST25.txt

Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu Gln Ala Ile Ser Phe
100 105 110

Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val His Asp Glu Ile Glu
115 120 125

Val Ala Gln Phe His Asp Lys Val Gly Lys Leu Tyr Tyr Tyr Leu Gly
130 135 140

Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln Ala Met Glu Ile Phe
145 150 155 160

Lys Gly His Gly Asp His Asp Met Asn Leu Val Ser Thr Tyr Ile Thr
165 170 175

Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr Thr Glu Ala Glu Glu
180 185 190

Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys Ala Gly Asp Cys Phe
195 200 205

Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu Leu Tyr Ala Ala Met
210 215 220

Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu Ile Val Leu Asp Asp
225 230 235 240

Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn Ala Val Phe Leu Met
245 250 255

Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys Arg Ala Ala Ala Phe
260 265 270

Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala Ala Asn Lys Ile Phe
275 280 285

Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr Ala Gly Asp Gly Glu
290 295 300

Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu Ile Leu Phe Gln Thr
305 310 315 320

Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val
325 330 335

Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu
340 345 350

Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met
355 360 365

10295.204.ST25.txt

<210> 37
<211> 1936
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (384)..(1433)

<400> 37	60
taatgaagca aaaccgggga gcaaatggc gattgaaaca gagatgaacc ttgttcacg	
catcattcaa gaacatcctg ataaacaaat cgaatccctt aaccctgata tgtgtccttg	120
tttgacaatg aacagaatcg acatgccgca tttgctgtgg tcgctggagc agatcgacaa	180
aggtgaacctg acaggcgtga tcaaagtgg acaagatatt gcaaaagatg ccattcttgc	240
gctgaatcgg atgtaacga tccgttaact ttttggagaa caagtttta tcataacccc	300
tccgctatgc gcataaaattt gtggagaagc atatttgtta ttctcatctg ttgttcacg	360
ttttgcata ggaggggaaa acg ttg aaa att cat att gtc caa aag ggc gat	413
Leu Lys Ile His Ile Val Gln Lys Gly Asp	
1 5 10	
tct ctg gaa aaa atc gcg gaa aga tat gaa gtg gac ttt gaa gaa ctg	461
Ser Leu Glu Lys Ile Ala Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu	
15 20 25	
aaa aag ctg aat tcg cag ctg agc aat cca gac ttg atc atg ccg ggc	509
Lys Lys Leu Asn Ser Gln Leu Ser Asn Pro Asp Leu Ile Met Pro Gly	
30 35 40	
atg aaa atc aaa gta ccg tca ggg gga gtg ccg gtc aaa aaa gaa gaa	557
Met Lys Ile Lys Val Pro Ser Gly Gly Val Pro Val Lys Lys Glu Glu	
45 50 55	
cag ctc aat atg cga aag gaa tta ccg aaa aaa cag cag gaa cat cca	605
Gln Leu Asn Met Arg Lys Glu Leu Pro Lys Lys Gln Gln Glu His Pro	
60 65 70	
ttt gca aaa gaa aag ccg aaa agc aag ctt gat gtt gaa gat ata aaa	653
Phe Ala Lys Glu Lys Pro Lys Ser Lys Leu Asp Val Glu Asp Ile Lys	
75 80 85 90	
ccg aaa gaa aag cct tcg gtt cct tat gtt ccg cct gtc ccg aac atc	701
Pro Lys Glu Lys Pro Ser Val Pro Tyr Val Pro Pro Val Pro Asn Ile	
95 100 105	
gga caa tca agt ttg cct gaa ggc gac att tcg aat ttg tat caa agc	749
Gly Gln Ser Ser Leu Pro Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser	
110 115 120	
gtc aat cag ctt cat cag ccg tac gta cct cca aaa cct tat gaa cat	797
Val Asn Gln Leu His Gln Pro Tyr Val Pro Pro Lys Pro Tyr Glu His	
125 130 135	
caa gag aaa ggc ccc aac atg tat aat cca tgg aca aat gag gag gaa	845
Gln Glu Lys Gly Pro Asn Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu	
140 145 150	
aac cat atg gaa aat gtc aat tat ccg aat gtt ccg cag ccg cca aat	893
Asn His Met Glu Asn Val Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn	
155 160 165 170	
gtc ggt gca gca ggt gat gaa aat aag cag ttt cac ggc atg ccg aat	941

10295.204.ST25.txt

val Gly Ala Ala Gly Asp Glu Asn Lys Gln Phe His Gly Met Pro Asn
175 180 185

gta gct gca gcg gga tat cat cac cat cca tat cct tat ccg ttc tat 989
Val Ala Ala Ala Gly Tyr His His His Pro Tyr Pro Tyr Pro Phe Tyr
190 195 200

cct gga ggc tgc tgg att cct gtt tca ccc gtg ctg cct gga tcg gga 1037
Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly
205 210 215

ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat 1085
Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His
220 225 230

cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg 1133
Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met
235 240 245 250

ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act 1181
Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr
255 260 265

gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca 1229
Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro
270 275 280

aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat 1277
Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp
285 290 295

gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg 1325
Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala
300 305 310

gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg 1373
Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly
315 320 325 330

gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa 1421
Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu
335 340 345

gat gat gaa gac tgattcgaa tgggacgatg atctatcgat ccttttttat 1473
Asp Asp Glu Asp
350

tgtggaccgc tataaacatt ttcatgctat ttaacggaa tgtctataac tgtcaagggt 1533

aactcttcgc atccccaca tcctaaaaaa gagcgcaatg ctcaaattca gcggtttca 1593

cgggggtac taccattgga cagcaagctg aaagtgttt cgggatattt gctttgaca 1653

gcaggtctat ctgcattgcgg aacgaacgac gctatagata atggaaacaa tacgcgccc 1713

atcgatatt atctcaaattg atgcagatcg taatgcaggg tcttgataat gacggccctg 1773

ttacagaaat gcttggaaac atgaacggaa gacacgggtc aacaaacgta aacaatcgag 1833

cgggaaacgg caatcccggtt ccaacaggcg atggaactta cagccgggaa gacatgaatt 1893

atcacaacca tttggtaat acggcggata caggctatga cag 1936

<210> 38
<211> 350
<212> PRT
<213> Bacillus licheniformis

10295.204.ST25.txt

<400> 38

Leu Lys Ile His Ile Val Gln Lys Gly Asp Ser Leu Glu Lys Ile Ala
1 5 10 15

Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu Lys Lys Leu Asn Ser Gln
20 25 30

Leu Ser Asn Pro Asp Leu Ile Met Pro Gly Met Lys Ile Lys Val Pro
35 40 45

Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys
50 55 60

Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro
65 70 75 80

Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser
85 90 95

Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro
100 105 110

Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln
115 120 125

Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn
130 135 140

Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val
145 150 155 160

Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp
165 170 175

Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr
180 185 190

His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile
195 200 205

Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr
210 215 220

Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser
225 230 235 240

Pro Ala Glu Tyr Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly
245 250 255

His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro
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10295.204.ST25.txt
260 265 270

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly
275 280 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro
290 295 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met
305 310 315 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro
325 330 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp
340 345 350

<210> 39
<211> 2027
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1526)

<400> 39 aagagcaaat tctgtctatg agcacaacag aagagggtgt acaattcgta aaagaaacct tcaaacctggc ataaagcaatt gaaaatccgg accggcatca ccaatgcccc tccgggtttt ttgttttatct gaatgtatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa gggggattct gatatgccta ggcagccatt caaaactggga gatgagggtgt atgtcattta ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtgc ttgatcatcc gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct ttgccgaaga tgatgcgcgtt tttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg gatatgaaga cattaccggc atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr 1 5 10	60 120 180 240 300 360 420 480 533
--	--

att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp 15 20 25	581
--	-----

aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn 30 35 40	629
--	-----

cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn 45 50 55	677
--	-----

gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp	725
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10295.204.ST25.txt

60	65	70	75	
tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt				773
Ser Ser Lys Pro Ser Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys				
80	85		90	
atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag				821
Met Gly His Cys His Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys				
95.	100		105	
ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg				869
Pro Tyr Ile Arg Thr Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala				
110	115		120	
gat caa tat ata aaa gaa agg gct ccc gaa gat acg cggtt gaa gct				917
Asp Gln Tyr Ile Lys Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala				
125	130		135	
tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta				965
Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu				
140	145		150	155
aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt				1013
Lys Arg Ala Ile Glu His Phe Gly Gln Thr Asp His Gly Lys Leu Arg				
160	165		170	
ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac				1061
Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His				
175	180		185	
aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att				1109
Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile				
190	195		200	
aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cggtt atc gaa gcc				1157
Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala				
205	210		215	
gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttatc atc atc gct				1205
Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala				
220	225		230	235
ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg				1253
Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu				
240	245		250	
gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc				1301
Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr				
255	260		265	
ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att				1349
Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile				
270	275		280	
gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cggtt				1397
Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg				
285	290		295	
cgc tat aaa tgg ggc aga tac ggg att ggc aaa tac att tat cag aag				1445
Arg Tyr Lys Trp Gly Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys				
300	305		310	315
gat gaa gaa gca gag ctt cgc agc gcc ctt gaa tcg tat atc gac aac				1493
Asp Glu Glu Ala Glu Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn				
320	325		330	
tat ttt ccc gaa gca aaa atc gaa tat ttc aca taacagagct ttagttgata				1546
Tyr Phe Pro Glu Ala Lys Ile Glu Tyr Phe Thr				

10295.204.ST25.txt
340

aagctctgtt	ttttgttttg	aaaacattat	gttaaaaaag	gattttcca	ctccattaac	1606
accgcataat	caagcgattc	ctcatcttca	atgtagccgg	gaatcacaca	aactggagag	1666
cgtccgcaat	gaagcaggaa	cgagagcact	ggatcgcgt	tttccccgtc	caatacagct	1726
tgaacatact	gttcgggcgt	catttcttca	gccgacttgt	gataatgggg	aatccgtccg	1786
ccgccaatga	gacgcttgag	ccctttaag	accgtcagtt	catacatgga	ttgcatcagc	1846
cgcattccga	tgccgagttt	tcgatagtcg	ggggacacgg	aaatatcgac	gacataaagg	1906
gagtttccat	cgttttgatg	tgtgccata	tacccgttgt	ccgtcacttc	atcccagctg	1966
tggtgccgat	gatgcggatc	aaaatcagcc	atgagcgctg	tcatcgaacc	gatgatgcgg	2026
c						2027

<210> 40

<211> 342

<212> PRT

<213> **Bacillus licheniformis**

<400> 40

Met	Val	Lys	Pro	Phe	Val	Pro	Gln	Leu	Val	Tyr	Ile	Glu	Pro	Arg	Ala
1					5				10			15			

Leu	Glu	Tyr	Pro	Leu	Gly	Lys	Glu	Leu	Arg	Asp	Lys	Phe	Ser	Asn	Met
							25					30			

Gly	Leu	Glu	Ile	Arg	Glu	Thr	Thr	Ser	His	Asn	Gln	Val	Arg	Asn	Ile
					35		40				45				

Pro	Gly	Glu	Gly	His	Leu	Gln	Lys	Tyr	Arg	Asn	Ala	Lys	Ser	Thr	Leu
					50		55				60				

val	Ile	Gly	Val	Arg	Lys	Thr	Leu	Lys	Phe	Asp	Ser	Ser	Lys	Pro	Ser
65					70			75						80	

Ala	Glu	Tyr	Ala	Ile	Pro	Phe	Ala	Thr	Gly	Cys	Met	Gly	His	Cys	His
								85	90				95		

Tyr	Cys	Tyr	Leu	Gln	Thr	Thr	Met	Gly	Ser	Lys	Pro	Tyr	Ile	Arg	Thr
							100				105		110		

Tyr	Val	Asn	Val	Glu	Glu	Ile	Leu	Glu	Gln	Ala	Asp	Gln	Tyr	Ile	Lys
							115		120			125			

Glu	Arg	Ala	Pro	Glu	Asp	Thr	Arg	Phe	Glu	Ala	Ser	Cys	Thr	Ser	Asp
						130		135			140				

Ile	Val	Gly	Ile	Asp	His	Leu	Thr	His	Thr	Leu	Lys	Arg	Ala	Ile	Glu
							145		150		155		160		

10295.204.ST25.txt

His Phe Gly Gln Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe
 165 170 175

His His Val Asp His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg
 180 185 190

Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro
 195 200 205

Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala
 210 215 220

Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His
 225 230 235 240

Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg
 245 250 255

Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln
 260 265 270

His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro
 275 280 285

Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly
 290 295 300

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu
 305 310 315 320

Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn Tyr Phe Pro Glu Ala
 325 330 335

Lys Ile Glu Tyr Phe Thr
 340

<210> 41

<211> 905

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(905)

<400> 41 acaaatacag tacaggccgg gaagacggga tatacaaggc ttgcaaagcg gacgctcgtc 60

tccatttcat cgaaagacgg aaccgatttg atcgccgtca caatcaatgc ccctgacgac 120

tggaatgatc atatgaacat gttcaactat gtattcgccc agtacaaaac atatatcatc 180

gccaaaaaaag gcgagattcc gaaattaaaa gactctttt acggacatac agcttttatt 240

aacggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa ggttgatatc 300

10295.204.ST25.txt

gagcttcttg aaccgaaaaa atcatggcgt aaaaacaaaa aagaaatccc ggacatcatc	360
ggagaaatga acgtcatgtt cgacggaaaa acgattgcaa gcgtaccgat ctattatgaa	420
aacgagcgaa acaaaaatcc gaaaaaatcg ttttcgaga ccttcaatc cgtattccaa	480
aaagcggcgg gcggttcatc atg gtc aat ata atc tgg gtc ggc tta acg gtg Met Val Asn Ile Ile Trp Val Gly Leu Thr Val	533
1 5 10	
atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn	581
15 20 25	
gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly	629
30 35 40	
ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu	677
45 50 55	
cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile	725
60 65 70 75	
tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr	773
80 85 90	
att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala	821
95 100 105	
aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac ccg Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg	869
110 115 120	
aac cgc agg gaa gcg agc cgc tca atg cac cca ggc Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly	905
125 130 135	

<210> 42
<211> 135
<212> PRT
<213> Bacillus licheniformis

<400> 42
Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe
1 5 10 15

Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys
20 25 30

Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu
35 40 45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu
50 55 60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro
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10295.204.ST25.txt

65

70

75

80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu
 85 90 95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile
 100 105 110

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala
 115 120 125

Ser Arg Ser Met His Pro Gly
 130 135

<210> 43
 <211> 1568
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1076)

<220>
 <221> CDS
 <222> (1112)..(1567)

<400> 43
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 actctgaagc gaagcgcccta ggtgctaaac gtgcagacgg tcaattcgta tctggccgtt 120
 caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc 180
 gatattacac tctatttgca aaagtcgacg gaactgttaa attcgaacct ttcggccgt 240
 cccccaaaaa agtgagcgta tatcctgttag cctaaccctt aaacgaaact ccggtcgttc 300
 tgaccggagt ttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa 360
 ataaggccgg gtttccgctc tgattctgtc tcgttaaagt atataaacgt gtttcattta 420
 tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc 480
 aaacgattgg gagtgccaaa atg gaa gaa act tcg aaa aaa cga gaa aag aat 533
 Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn
 1 5 10

atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac 581
 Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His
 15 20 25

tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta 629
 Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu
 30 35 40

aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc 677
 Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val
 45 50 55

atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc 725
 Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg

10295.204.ST25.txt

60	65	70	75	
gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr 80 85 90				773
ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu 95 100 105				821
gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp 110 115 120				869
gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr 125 130 135				917
gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val 140 145 150 155				965
ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp 160 165 170				1013
ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala 175 180 185				1061
gaa att cat atc aag taaagcggtt ttttaggaat agaacggagg acatt atg Glu Ile His Ile Lys 190				1114
ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn 195 200 205				1162
ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro 210 215 220 225				1210
gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac Ala Gly Gly Asp Gly Lys Gly Gly Asp Val Val Phe Lys Val Asp 230 235 240				1258
gaa ggt ctc acg acg ctg atg gat ttt aga tat caa aga cat ttt aag Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys 245 250 255				1306
gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn 260 265 270				1354
gcc gaa gac atg gtt gtg aaa gtc ccc ggc acg gtt gtc att gac Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp 275 280 285				1402
gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu 290 295 300 305				1450
gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt Ala Val Ile Ala Lys Gly Gly Arg Gly Arg Gly Asn Thr Arg Phe 310 315 320				1498
gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro				1546

10295.204.ST25.txt

325

330

335

1568

ggc aag gag cgc tat att gtt c
Gly Lys Glu Arg Tyr Ile Val
340

<210> 44

<211> 192

<212> PRT

<213> *Bacillus licheniformis*

<400> 44

Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn Met Asp Asp Lys Ala
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20 25 30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr
35 40 45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His
50 55 60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu
65 70 75 80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val
85 90 95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val
100 105 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly
115 120 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp
130 135 140

Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr
145 150 155 160

Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys
165 170 175

Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys
180 185 190

<210> 45

<211> 152

<212> PRT

<213> *Bacillus licheniformis*

<400> 45

10295.204.ST25.txt

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
 1 5 10 15

Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
 20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
 35 40 45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
 50 55 60

Lys Ala Ala Arg Gly Glu His Met Ser Lys Asn Gln His Gly Arg
 65 70 75 80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
 85 90 95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
 100 105 110

Glu Ala Val Ile Ala Lys Gly Arg Gly Arg Gly Asn Thr Arg
 115 120 125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
 130 135 140

Pro Gly Lys Glu Arg Tyr Ile Val
 145 150

<210> 46
 <211> 1849
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1346)

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agtccggctg aaaagggttt tggaatcggt caaacaaaac tatgatttca tgattattga	120
ctgccccccg tcattagggc tgcttacaat caatgcgtt acggcttccg attccgtcgt	180
gattccggtc cagtgcgagt attatgcgtt ggaagggttg agccagctgc tcaactctgt	240
ccggctcgtg caaaaacatt taaatacgga tctgatgatc gacggcgtat tgctgacaat	300
gcttcatgca agaacgaatt taggcataca ggtcatcgaa gaagtaaaaa agtacttccg	360
cgataaagta tacaaaacgg ttatcccccg gaatgtccgg ctcagtgaag cgccgagtca	420
tggaaagccg atcattttat atgatccccg ttccagagga gcgaaagtct atttagaatt	480

10295.204.ST25.txt

agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala	533
1 5 10	
ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys	581
15 20 25	
ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp	629
30 35 40	
gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val	677
45 50 55	
ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtc Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val	725
60 65 70 75	
gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr	773
80 85 90	
att cct gcg att gtc cgc gag ctg tcg gaa tcc ctg atg atg gag att Ile Pro Ala Ile Val Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile	821
95 100 105	
gcc cta ttg gaa aat ctt caa cga gaa gac ctg tct ccg ctt gaa gaa Ala Leu Leu Glu Asn Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu	869
110 115 120	
gca aaa gcc tat gaa tct ttg ctc aaa cat ctc gat atg acc cag gaa Ala Lys Ala Tyr Glu Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu	917
125 130 135	
cag ctg gcg aaa agg ctt gga aaa agc agg cct cac atc gcc aac cac Gln Leu Ala Lys Arg Leu Gly Lys Ser Arg Pro His Ile Ala Asn His	965
140 145 150 155	
ttg cgg ctg aca ctt cct gaa gac gtt caa aag tta atc gac aac Leu Arg Leu Leu Thr Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn	1013
160 165 170	
ggc acg tta tcg atg ggc cat ggc cga aca ttg ctt gga ttg aaa aac Gly Thr Leu Ser Met Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn	1061
175 180 185	
aag aaa aag ctt gag ccg ctt gtt caa aag gtc gtg tcc gaa cag ttg Lys Lys Leu Glu Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu	1109
190 195 200	
aac gtc cgc cag ttg gaa aag tta att caa cag ttg aac gct gat gtt Asn Val Arg Gln Leu Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val	1157
205 210 215	
cca cgt gaa aca aag aag ccg aaa caa gtc aaa gat gca gtg atc aag Pro Arg Glu Thr Lys Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys	1205
220 225 230 235	
gaa cgg gaa tcg tat ttg cga aac tat ttt gga aca ccg gtg acc att Glu Arg Glu Ser Tyr Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile	1253
240 245 250	
aaa aag caa aag aaa aaa ggc agg atc gaa atc gaa ttc tac tca aat Lys Lys Gln Lys Lys Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn	1301
255 260 265	

<210> 47
<211> 282
<212> PRT
<213> *Bacillus licheniformis*

<400> 47

Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala Leu Phe Ser Asn Val
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Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys Leu Gln Asp Leu Arg
20 25 30

Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp Asp Gln Ser Leu Lys
35 40 45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile
50 55 60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg
65 70 75 80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val
85 90 95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn
100 105 110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu
115 120 125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg
130 135 140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr
145 150 155 160

10295.204.ST25.txt

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met
165 170 175

Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu
180 185 190

Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu
195 200 205

Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys
210 215 220

Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr
225 230 235 240

Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile Lys Lys Gln Lys Lys
245 250 255

Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg
260 265 270

Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
275 280

<210> 48
<211> 3490
<212> DNA
<213> *Bacillus licheniformis*

<220>
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<222> (501)..(2987)

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agaaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacgggtc ataccggta	240
ggtcgggggt tcgatcccct ccgcccgtac ttatatgaag gcccgttggt caagtggta	300
agacaccgccc cttcacggc ggtAACACGG gttcgaatcc cgtacgggtc attccggaaa	360
ccggcttctt ctgaagccgg tttttgctg cataaaaaata tgcaaaataa cggaaatgga	420
ctcgacttat caagagtgtat tgaagcatgc tacaaaaaagc gtcgaacagt tctttgaatt	480
cgttacccctc ttttgacaaa atccctatttc atctttcgct ataatggcaa gcaacgaata	533
aacgagtgccc agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca	581
Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro	
1 5 10	

ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg	581
Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met	
15 20 25	

10295.204.ST25.txt

acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Tyr Lys Gly 30 35 40	629
ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu 45 50 55	677
tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu 60 65 70 75	725
atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly 80 85 90	773
gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu 95 100 105	821
ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp 110 115 120	869
cgt gtc aga acg ctg cct gtc gtc ttt ttg gcg atg gct gtg aca Arg Val Arg Thr Leu Pro Val Val Phe Leu Ala Met Ala Val Thr 125 130 135	917
aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His 140 145 150 155	965
tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu 160 165 170	1013
att ttt ctg caa agc ctg ccg att gtc aca tca aag cgg gcg aaa cag Ile Phe Leu Gln Ser Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln 175 180 185	1061
tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc Ser Leu Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser 190 195 200	1109
gtt ctc acg ggc ttg aca ggc gtt tca ttt caa ggc atg cag gct gaa Val Leu Thr Gly Leu Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu 205 210 215	1157
ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly 220 225 230 235	1205
gca agc atc ggc tgt aca gtc ggg gtt gtg acc ggg ctg att ctc agc Ala Ser Ile Gly Cys Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser 240 245 250	1253
ctc tca aac atc ggc aat tta tat cag atg agc ctg ctg gct ttc tca Leu Ser Asn Ile Gly Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser 255 260 265	1301
ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala 270 275 280	1349
gtc ggc tta ttg att gga tct cta ttg att tct ctg tac gga gaa ggt Val Gly Leu Leu Ile Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly 285 290 295	1397

10295.204.ST25.txt

tcg gct gaa tta gtg ccg acg ctt tat gaa tct ctg att gca atc ggc Ser Ala Glu Leu Val Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly 300 305 310 315	1445
ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr 320 325 330	1493
ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg Ile Pro Gly Thr Thr Glu His Ala Gln Glu Gln Gln Tyr Ala Arg 335 340 345	1541
aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val 350 355 360	1589
ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro 365 370 375	1637
gac gat gaa gga aaa gaa aaa gag atc gat ctg ttt ttg agc acg gtg Asp Asp Glu Gly Lys Glu Ile Asp Leu Phe Leu Ser Thr Val 380 385 390 395	1685
aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val 400 405 410	1733
cag aac ttt gat aaa aca tat gat ttg atg aaa cggtt atg cag gaa Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu 415 420 425	1781
acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe 430 435 440	1829
cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac His Gln His Cys Ser Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp 445 450 455	1877
gag ctg act cat ttt agg gcg aac cag aca tta aaa caa aag gtg cat Glu Leu Thr His Phe Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His 460 465 470 475	1925
gac agc aga cgt ctc gtt gca gag cag ctt ctc ggc gtt tct cag gtt Asp Ser Arg Arg Leu Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val 480 485 490	1973
atg gcg gac ttt tct cgg gaa ata aaa agg gaa agg gag cag cat ttt Met Ala Asp Phe Ser Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe 495 500 505	2021
att caa gaa gag caa att cgg gat gcg ctg cag cac ttc ggc atc gag Ile Gln Glu Gln Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu 510 515 520	2069
att cag caa gtc gaa ata tac agc ctt gag cag gga aac atc gat att Ile Gln Gln Val Glu Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile 525 530 535	2117
gaa atg agt atc ccg tat tgc aac ggc cat gga gag tgt gaa aaa atc Glu Met Ser Ile Pro Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile 540 545 550 555	2165
atc gct ccg atg ctg tcc gat att ttg gaa gaa caa att atc gtc aaa Ile Ala Pro Met Leu Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys 560 565 570	2213

10295.204.ST25.txt

gca gaa cag tgc gcc ggc cat ccg aat gga tat tgt cat gtt gcc ttc Ala Glu Gln Cys Ala Gly His Pro Asn Gly Tyr Cys His Val Ala Phe 575 580 585	2261
ggt tcg gcg aag tca tac agg gtg gtg aca gga gcc gcg cat gca gca Gly Ser Ala Lys Ser Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala 590 595 600	2309
aaa ggc gga ggg ctt gtc tcc ggc gac agc tac aat atg atg gag ctc Lys Gly Gly Leu Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu 605 610 615	2357
ggc acc ggc aaa tat gcc gcc att agc gat ggt atg gga aat ggc Gly Thr Gly Lys Tyr Ala Ala Ile Ser Asp Gly Met Gly Asn Gly 620 625 630 635	2405
gca agg gcc cat ttt gaa agc aat gag acg atc aag ctg ctg gaa aag Ala Arg Ala His Phe Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys 640 645 650	2453
att ctt cag tcg ggc atc gac gaa aaa gtg gcg att aaa acg att aac Ile Leu Gln Ser Gly Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn 655 660 665	2501
agc att ctt tca tta agg aca aca gat gaa att tat tcg aca ttg gat Ser Ile Leu Ser Leu Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp 670 675 680	2549
tta tcg gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile 685 690 695	2597
ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val 700 705 710 715	2645
cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat Gln Ala Ser Asn Leu Pro Ile Gly Ile Thr Glu Phe Asp Val Asp 720 725 730	2693
gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser 735 740 745	2741
gac gga atc ttt gaa ggg ccg aga cat gtg gaa aat cat gat ctg tgg Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp 750 755 760	2789
atg aag cgc aaa ttg aaa tcg ctg aaa acc gag gag ccg cag gaa atc Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile 765 770 775	2837
gcc gac tta atc atg gaa gaa gtg atc ccg aca agg tcg ggt ctg att Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile 780 785 790 795	2885
gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro 800 805 810	2933
aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu 815 820 825	2981
att tct tagcattcgt ataaaatcaa tttcttctgg cgatgatgga actaaatcaa Ile Ser	3037

10295.204.ST25.txt

gatatcttg tccaggagga ataaaaacga tggaaaagg gcatttgaat caaatcctgc	3097
tttgacgga cggctgttca aaccgcggcg aagacccgca ggccatggct gccttcgca	3157
aagagcaggg aattaccgtg aatgtgattt ggattatgga cgagcatgaa atggatcagg	3217
aggcgatgaa agaagtcgaa gggatcgctc tcgcaggcgg aggagttcac caggtggttt	3277
acacgtcgcgca gctgtcgcag accgttcaaa tggtgacaaa aaaggcgatg acgcaaacc	3337
ttcaaggcgt ggtcaacagt gagctcaaac aaattctcgg caagcatacc gaaatggatg	3397
aactgcctcc tgataaacgc ggtgaagtca tggaaagtcgt tgacgagctt ggtgagaccg	3457
tgcatcttca tgtactggtt cttgtcgata caa	3490

<210> 49

<211> 829

<212> PRT

<213> *Bacillus licheniformis*

<400> 49

Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro Ile Ala Gly Pro Ala			
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Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met Thr Lys Leu Met Met		
20	25	30

Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val		
35	40	45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro		
50	55	60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys			
65	70	75	80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser		
85	90	95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile		
100	105	110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu		
115	120	125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val		
130	135	140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe			
145	150	155	160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser		
165	170	175

10295.204.ST25.txt

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu
180 185 190

Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu
195 200 205

Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg
210 215 220

Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys
225 230 235 240

Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly
245 250 255

Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly
260 265 270

Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile
275 280 285

Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val
290 295 300

Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr
305 310 315 320

Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr
325 330 335

Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val
340 345 350

Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser
355 360 365

Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys
370 375 380

Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys
385 390 395 400

Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys
405 410 415

Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln
420 425 430

Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser
435 440 445

10295.204.ST25.txt

Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe
450 455 460

Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu
465 470 475 480

Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser
485 490 495

Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln
500 505 510

Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu
515 520 525

Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro
530 535 540

Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu
545 550 555 560

Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala
565 570 575

Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser
580 585 590

Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Leu
595 600 605

Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr
610 615 620

Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe
625 630 635 640

Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly
645 650 655

Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu
660 665 670

Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp
675 680 685

Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser
690 695 700

Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu
705 710 715 720

10295.204.ST25.txt

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln
 725 730 735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu
 740 745 750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu
 755 760 765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met
 770 775 780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr
 785 790 795 800

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile
 805 810 815

Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu Ile Ser
 820 825

<210> 50
<211> 1928
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1427)

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ttcaaaaccg ctgccccaaaa cgtaacggag ctgccgatca gagaagtctc aaaaggaaaa		180
tatgaaggat attggaccgc tacttcaact gcaaaagcaa aaggagcgg aatcgaggtc		240
atcgtcagag atgattacgg caatgaaaacg agacaaaacgg caaaaggcaa gctgtatatc		300
aatgaaaagc taaaaataaag gtgaaaagac gctgtctta atggcagcgt ttttttcgtt		360
ttacgatcga caaattcagt acgaaaactt caaaaaatgt acgatttacg caacattaat		420
tgacagactt tacctttggg cttgatttat acttagaaaa acaaacaacta aggtcaccga		480
gccgcagaaa ggggaaggat gtg gaa atc tat tta gat gcg ata tgg ctg tta		533
Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu		
1 5 10		
aac ttt tgt ttt gac ttg ctg ctt tta atg atg acc gca ttt att tta		581
Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu		
15 20 25		
aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg		629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala		
30 35 40		

10295.204.ST25.txt

tca agc atc gtt ctg ttt atg ttt aca cct ttt tca ccg tac gtc ctt Ser Ser Ile Val Leu Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu 45 50 55	677
cat cct gcc ggc aaa ctg tcg ttt tcg gtt gtg atc gtt ctt gtg gca His Pro Ala Gly Lys Leu Ser Phe Ser Val Val Ile Val Leu Val Ala 60 65 70 75	725
ttt ggt ttt aag cgg ttc cgg ttt ttt ttg cag aat ttg ttt tct ttt Phe Gly Phe Lys Arg Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe 80 85 90	773
tat ttt gcc act ttt tta atg gga gga ggg att atc gga gcg cat tct Tyr Phe Ala Thr Phe Leu Met Gly Gly Ile Ile Gly Ala His Ser 95 100 105	821
ttg ctt gaa acg gat tcg atc atg gaa aac ggc gtc ttt atg acg aat Leu Leu Glu Thr Asp Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn 110 115 120	869
tgg tcc ggt ttt gga gac ccc gtc agc tgg ctg ttt gtc tgt gtg ggt Trp Ser Gly Phe Gly Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly 125 130 135	917
ttt gcg gct gta tgg ctg ttt tca aaa aag cgt ttt gaa gat gct gaa Phe Ala Ala Val Trp Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu 140 145 150 155	965
gcg aag aaa att caa tac gaa gaa cgc gtc cgc cta gag gcc tgc att Ala Lys Lys Ile Gln Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile 160 165 170	1013
ggg gaa cat acg ctt cat ttc acc gga ttg att gac tcc gga aac cag Gly Glu His Thr Leu His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln 175 180 185	1061
ctc tac gat cca atc aca aaa acg ccc gtc atg atc gtc aat att gaa Leu Tyr Asp Pro Ile Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu 190 195 200	1109
aaa ttg aaa gtt gta ttg gga gaa gag gca agt gtg acc atc aag gaa Lys Leu Lys Val Val Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu 205 210 215	1157
atg agc ccg ctt gat gcc gtc ggg aaa ctg gat gaa gca ctg ccg tat Met Ser Pro Leu Asp Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr 220 225 230 235	1205
atc ggg cgg atc cgc ctg att ccg tac cgc ggg gtc ggc cat cag cat Ile Gly Arg Ile Arg Leu Ile Pro Tyr Arg Gly Val Gly His Gln His 240 245 250	1253
cag ttt ctg ctc tgc tta aag ccg gat cat gtg ctc gtt tgt acg gaa Gln Phe Leu Leu Cys Leu Lys Pro Asp His Val Leu Val Cys Thr Glu 255 260 265	1301
aga gaa gtg att gaa gcg ccg aaa tgc ctg att ggc atc acg aca tca Arg Glu Val Ile Glu Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser 270 275 280	1349
ccg ctt tcc gct gac ggc gaa ttt gac gcc atc gtc cat ccg aaa atg Pro Leu Ser Ala Asp Gly Glu Phe Asp Ala Ile Val His Pro Lys Met 285 290 295	1397
ctg gcc gga aac ccg gtc aaa cac gtt tct taaacttgaa gtctgttaca Leu Ala Gly Asn Pro Val Lys His Val Ser 300 305	1447

10295.204.ST25.txt
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aggtaacct atctatggta caaacTTTA atgaaactgg ggctgaaaag cgacgaaatt 1567
tattatATCG gcggAAAGCgA ggcgCTTCCC ccGCCATTGT caaaAGATGA agAGCAGGtG 1627
cttctccata agctgcCTGA cggtgatcag gcccACGAG cgatttGat tGAACGAAAT 1687
ctcagactgg tcgtgtacat cgcgagaaaa tttgAAAATA cagGAATCAA tatcgaggat 1747
ttaatCTCCA tcggcacGAT cgggCTCATC aaAGCggTGA atacGTTAA tcccGAGAAA 1807
aaaatcaaAC tggctacata tgcttCCAGA tgCATTGAAA atGAAATTT GATGTATTa 1867
agaagaaaca ataaaATCCG ttCAgAGGta tcattcGAcG aaccGCTGAA catcgattGG 1927
1928

g

<210> 51
<211> 309
<212> PRT
<213> *Bacillus licheniformis*

<400> 51

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20 25 30

Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu
35 40 45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys
50 55 60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg
65 70 75 80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe
85 90 95

Leu Met Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp
100 105 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly
115 120 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp
130 135 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln
145 150 155 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu
165 170 175

10295.204.ST25.txt

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile
 180 185 190

Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val
 195 200 205

Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp
 210 215 220

Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg
 225 230 235 240

Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys
 245 250 255

Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu
 260 265 270

Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp
 275 280 285

Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro
 290 295 300

Val Lys His Val Ser
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<210> 52
 <211> 1922
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1421)

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taagatcatg aagctttct ttggacaagt caatccgacg gtttgacaa tggcggcg	240
aagggtggta tcatcttga tcgaactgac ggcggctgtt gtatgtctt tgacaaacga	300
cgtcagaaaa gctgtggcg tcaacagcgt actggccatg gtcgggcccgc tcatctttat	360
tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat	420
tttgatcttt atgggagtgg tttgatcat cgccccatc tataaatagc gacacatgat	480
aagagaggcc gacttgtcat aatgtcttcc tttgatcata catttttata gaagacaagc	533
aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg	
Leu His His Ile Thr Glu Ile Leu Pro Asp Thr	
1 5 10	

10295.204.ST25.txt

atc aaa cgc gcg ctc agc ggt ctt ggc gac cat gaa atc gat cag ata Ile Lys Arg Ala Leu Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile 15 20 25	581
gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys 30 35 40	629
gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala 45 50 55	677
ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu 60 65 70 75	725
gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly 80 85 90	773
ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga Leu Ala Gly Arg Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg 95 100 105	821
gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile 110 115 120	869
tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr 125 130 135	917
ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp 140 145 150 155	965
ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys 160 165 170	1013
gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly 175 180 185	1061
ata ccg caa tat cgg ctc ggc gac cgg gca gac atc ctt gac gcc tgt Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys 190 195 200	1109
cca aaa gcg gaa ggg ctg atg atg atc aga tcg atg agt ccg gag Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu 205 210 215	1157
gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu 220 225 230 235	1205
ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly 240 245 250	1253
tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln 255 260 265	1301
gag cac ccg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly 270 275 280	1349

10295.204.ST25.txt

ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly	1397
285 290 295	
gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttattttgg Ala Ala Lys Arg Met Leu Ser Cys	1451
300 305	
cagcagccac atggacagga ttgaaatgg cgaagcctt cagggaaagg ccgaagcaaa	1511
tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac	1571
cgctccgtca ggcataaaaa cagatcgac accagcttac cgagccgtt gcctctttgt	1631
ttcagacatt tgcagaacag cttgaaaaag gcagcgcttc agcaggacg gcatggaaag	1691
acagcctgga gaaagtatgg cccgaaacgg ctcttaaaaaa gaaagaatac gagattttac	1751
ggcaattcgg cggaaacgctg ggccgtcatg atctgatttc tcagcaaaaa catatcaa	1811
tggcgtaac ccatttagag acagaggaag ctgaagcaaa tctcgccag gcgaaaaatg	1871
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<210> 53

<211> 307

<212> PRT

<213> *Bacillus licheniformis*

<400> 53

Leu His His Ile Thr Glu Ile Leu Pro Asp Thr Ile Lys Arg Ala Leu	
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Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile Glu Glu Ile Arg Val	
20 25 30	

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe	
35 40 45	

Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala Leu Leu Asn Arg	
50 55 60	

Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu Leu Lys Lys Gly	
65 70 75 80	

Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly Leu Ala Gly Arg Val	
85 90 95	

Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe	
100 105 110	

Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val	
115 120 125	

Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro	
130 135 140	

10295.204.ST25.txt

Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile
 145 150 155 160

Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp
 165 170 175

Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg
 180 185 190

Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly
 195 200 205

Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp
 210 215 220

Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His
 225 230 235 240

Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp
 245 250 255

Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe
 260 265 270

Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser
 275 280 285

Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met
 290 295 300

Leu Ser Cys
 305

<210> 54
 <211> 1511
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (498)..(1010)

<220>
 <221> CDS
 <222> (1036)..(1239)

<220>
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 <222> (1255)..(1509)

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 agttcggaa gcggcaacgc ccctgccaaa aaagtggga ttgttgacga aaggtctgaa 120

10295.204.ST25.txt

atcgaggct gtgttaaacgg cataccgcaa tatcggctcg ggcggcc agacatcctt	180
gacgcctgtc caaaagcgg aaggctgatg atgatgatca gatcgatgag tccggaggta	240
atgatcgccg atgagatcgg gagaatggaa gacgcagaag cgctcttgg agcggtccac	300
gcgggggtga ctgtcatcgt ttcggctcac ggctacacat atgcagatct cgccaggcgt	360
ccatcattga aaatgcttca agagcaccgg gttttgagc gaatcgtgg aacttccaga	420
aagaacggtc ccggcagcct gagccgcatt ctaaatggga acggagagcc gtcggggca	480
gcaaagagga tgttatc atg ctg aag ctt tta ggt gcc gtc ctt att ttg Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu 1 5 10	530
gca gca gcc aca tgg aca gga ttt gaa atg gcg aag cct ttc agg gaa Ala Ala Ala Thr Trp Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu 15 20 25	578
agg ccg aag caa atc cgc cag ctg ttg gcc gct ttg cag tct ttg gag Arg Pro Lys Gln Ile Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu 30 35 40	626
gct gaa atc atg tac ggg cat aca ccg ctc cgt cag gca tca aaa cag Ala Glu Ile Met Tyr Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln 45 50 55	674
atc gca cac cag ctt acc gag ccg gta gcc tct ttg ttt cag aca ttt Ile Ala His Gln Leu Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe 60 65 70 75	722
gca gaa cag ctt gaa aaa ggc agc gct tca gca ggg acg gca tgg gaa Ala Glu Gln Leu Glu Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu 80 85 90	770
gac agc ctg gag aaa gta tgg ccc gaa acg gct ctt aaa aag aaa gaa Asp Ser Leu Glu Lys Val Trp Pro Glu Thr Ala Leu Lys Lys Glu 95 100 105	818
tac gag att tta cgg caa ttc ggc gaa acg ctg ggc cgt cat gat ctg Tyr Glu Ile Leu Arg Gln Phe Glu Thr Leu Gln Arg His Asp Leu 110 115 120	866
att tct cag caa aaa cat atc aaa ctg gcg tta acc cat tta gag aca Ile Ser Gln Gln Lys His Ile Lys Leu Ala Leu Thr His Leu Glu Thr 125 130 135	914
gag gaa gct gaa gca aat ctc gcc cag gcg aaa aat gaa aaa atg gtc Glu Glu Ala Glu Ala Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val 140 145 150 155	962
aaa agc ctt gga ttt ttg acg gga ctg cta ctg att ctt cta ttg atg Lys Ser Leu Gly Phe Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met 160 165 170	1010
taatgaagag gggagcatac acgaa atg gga gta gac gta aat att att ttt Met Gly Val Asp Val Asn Ile Ile Phe 175 180	1062
caa att gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg Gln Ile Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu 185 190 195	1110
gat caa atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga Asp Gln Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly 200 205 210	1158

10295.204.ST25.txt

ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe 215 220 225	1206
caa aag ata aaa gct gtc ttt cta ttt caa gga tagggggct cactc att Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly Ile 230 235 240	1257
gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser 245 250 255	1305
ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val 260 265 270	1353
ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu 275 280 285	1401
atc att cggtg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met 290 295 300	1449
atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala 305 310 315 320	1497
gag ttt ggc gcc ca Glu Phe Gly Ala	1511

<210> 55

<211> 171

<212> PRT

<213> Bacillus licheniformis

<400> 55

Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu Ala Ala Ala Thr Trp 1 5 10 15
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Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile 20 25 30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr 35 40 45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu 50 55 60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu 65 70 75 80
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Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys 85 90 95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg 100 105 110
--

10295.204.ST25.txt

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys
115 120 125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala
130 135 140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe
145 150 155 160

Leu Thr Gly Leu Leu Ile Leu Leu Leu Met
165 170

<210> 56

<211> 68

<212> PRT

<213> *Bacillus licheniformis*

<400> 56

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1 5 10 15

Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
50 55 60

Leu Phe Gln Gly
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<210> 57

<211> 85

<212> PRT

<213> *Bacillus licheniformis*

<400> 57

Ile Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu
1 5 10 15

Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val
20 25 30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr
35 40 45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn
50 55 60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile
65 70 75 80

10295.204.ST25.txt

Ala Glu Phe Gly Ala
85

<210> 58
<211> 1207
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(704)

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	ccgtcaggca tcaaaaacaga tcgcacacca gcttaccgag ccggtagcct ctttgttca	180
	gacatttgca gaacagcttg aaaaaggcag cgcttcagca gggacggcat gggaaagacag	240
	cctggagaaa gtatggcccgg aaacggctct taaaaagaaa gaatacgaga ttttacggca	300
	attcggcgaa acgctgggcc gtcatgatct gatttctcag caaaaacata tcaaactggc	360
	gttaacccat tttagagacag aggaagctga agcaaatctc gcccaggcga aaaatgaaaa	420
	aatggtcaaa agccttggat ttttgacggg actgctactg attcttcttat tgatgtaatg	480
	aagagggggag catacacgaa atg gga gta gac gta aat att att ttt caa att	533
	Met Gly Val Asp Val Asn Ile Ile Phe Gin Ile	
1	5	10

gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg gat caa
 Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu Asp Gln
 .
 15 20 25

atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga ttc att
 Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile
 30 35 40 629

tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc caa aag
Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys
45 . 50 . 55

ata aaa gct gtc ttt cta ttt caa gga tagggggct cactcattga
Ile Lys Ala Val Phe Leu Phe Gln Gly
60 65

cttagtagat caggtctacg aaatcattcg gatgattgaa aaaatagctg ccaatgtccaa 904

catcaacatg atgtatgtcg aaacgatttt gaagattatc gggattgctt atattgcgga 964

atttggccccc caqctgacaa aggatgccgg acagggtgcg attgcttcga agatcgaatt 1024

ccaaaaatctcatct tagtcatggc tgcattttaaaccgtga ttatcgaaac 1084

ccatgtctta gtcagaaaagg aqgatttcct gagtgaagcg 1144

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10295.204.ST25.txt

1207

ttc

<210> 59

<211> 68

<212> PRT

<213> Bacillus licheniformis

<400> 59

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Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
 50 55 60

Leu Phe Gln Gly
 65

<210> 60

<211> 2153

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1703)

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 ccaccccttccct cagcttgatt gtgaaagagc aaaaaccgac gtttgctttt ttgattgtcg 180
 tttttgccgg ctgcacgatt ttttattct tagtagatca ggtctacgaa atcattcgga 240
 tgattgaaaa aatagctgcc aatgccaaca tcaacatgat gtatgtcgaa acgattttga 300
 agattatcgg gattgcttat attgcggagt ttggcgccca gctgacaaag gatgccggac 360
 agggtgtcgat tgcttcgaag atcgaattgg caggcaaaat cctcatctta gtcatggctg 420
 tgcctatttt aaccgtgatt atcgaaacga tcatcgact catcccttcc atgtcttagt 480
 cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc 533
 Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile 1 5 10

gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa 581
 Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu
 15 20 25

gcg gag ccg gct ggg gaa acc gct gca gaa gaa tcg gca gaa gcc att 629
 Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile

10295.204.ST25.txt

30	35	40	
gca aga gag cag gct gaa ggt ttg gaa cta gac cg	45	50	677
Ala Arg Glu Gln Ala Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe		55	
tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa	60	65	725
Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln		70	
aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct	80	85	773
Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro		90	
gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg	95	100	821
Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu		105	
gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc	110	115	869
Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys		120	
gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc	125	130	917
Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser		135	
aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc	140	145	965
Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu		150	
aac agc ttt cgg gtt gcc gtc aca tat gcg aat gaa gcg att cag acg	160	165	1013
Asn Ser Phe Arg Val Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr		170	
atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg	175	180	1061
Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met		185	
gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att	190	195	1109
Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile		200	
ctt ttt ctc atg aac acg agc ggc ttg ttt atc caa tat atc gtg ttg	205	210	1157
Leu Phe Leu Met Asn Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu		215	
ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg	220	225	1205
Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr		230	
gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg	240	245	1253
Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala		250	
atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg	255	260	1301
Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser		265	
gtt cag ggc gcc tca gcc gca gtg acg gac ggc att act ttg cgg acg	270	275	1349
Val Gln Gly Ala Ser Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr		280	
gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt	285	290	1397
Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe		295	
acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac			1445
Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Lys Asn			

10295.204.ST25.txt

300	305	310	315	
acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe	320	325	330	1493
ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala	335	340	345	1541
gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat Ala Val Leu Gln Pro Leu Gly Gly Pro Val Ile Ser Cys Leu Asp	350	355	360	1589
gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val	365	370	375	1637
tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn	380	385	390	1685
ctg acg atg atg atg aag tagggaggaa tgagatggaa tttctgacag Leu Thr Met Met Met Lys	400			1733
agtggctcac gaatattattt ctatatttc tgatggcgat cgtcatcgat atgcttctgc cgaattcgag catgcaaaaa tacgcggaaa tggtgatcg cctgctttg atcggtttaa				1793
tactgaaccc gatttctct ttattcagga cagatccgga tgtgattttt gagaagctta caaaaaacgg acaagttcag tcaaacgaaa taaaaaatca gctgaattca gaaaaaaaaag				1853
aaataacaagc ctcacaacaa gcatatatct tagaacagat ggctgttcaa ttggaaaaga acgcagaggg caggtttaca agcgacaaat acaagataga ccgagtcgag gtctttctg				1913
acagccagct gaaaacagag aaagacctca gtaagcatgc ggaagtctcg gtatttttgaa				1973
				2033
				2093
				2153

<210> 61
<211> 401
<212> PRT
<213> *Bacillus licheniformis*

<400> 61
Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile Gly Ile Val Cys Phe
1 5 10 15

Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu Ala Glu Pro Ala Gly
20 25 30

Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala
35 40 45

Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu
50 55 60

Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu
65 70 75 80

10295.204.ST25.txt

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys
85 90 95

Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu
100 105 110

Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu
115 120 125

Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala
130 135 140

Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val
145 150 155 160

Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile
165 170 175

Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly
180 185 190

Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn
195 200 205

Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu
210 215 220

Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val
225 230 235 240

Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala
245 250 255

Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser
260 265 270

Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr
275 280 285

Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp
290 295 300

Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu
305 310 315 320

Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile
325 330 335

Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Val Leu Gln Pro
340 345 350

10295.204.ST25.txt

Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp Val Ile Ser Lys Ser
 355 360 365

Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val Ser Leu Met Phe Phe
 370 375 380

Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn Leu Thr Met Met Met
 385 390 395 400

Lys

<210> 62
 <211> 1696
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1193)

<400> 62	60
cttgatcggtt gtaatactga acccgatctt ctctttattc aggacagatc cggatgttat	
ttttgagaag cttacaaaaaa acggacaagt tcagtcaaac gaaataaaaaa atcagctgaa	120
ttcagaaaaaa aaagaaaatac aagcctcaca acaagcatat atcttagaac agatggctgt	180
tcaattggaa aagaacgcag agggcagggt tacaagcgcac aaatacaaga tagaccgagt	240
cgaggtctct tctgacagcc agctgaaaac agagaaagac ctcagtaagc atgcggaagt	300
ctcggtattc ttgaaaccag catcgaaaaa aacggtccaa gccgtcgctc ctgtcgagat	360
caatacggac cggagctacc agtccatgca ggaaagagaa aagaaagaga cggggaaagt	420
cagagaacag cttagcaggca tctggaaat aagccccgac aagattacag ttcatatcga	480
agggggagaa cgaagcggca atg aat aaa aga acc tgg atc gaa aag ctg atc	533
Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile	
1 5 10	
ggc cac ctc ccg aaa gac gag aaa gac gga aaa aag ctg acg aaa	581
Gly His Leu Leu Pro Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys	
15 20 25	
tat cac tac ttt ctg ctg ctt ttt gtt ctc ggc gtt tcc ttc atg ctc	629
Tyr His Tyr Phe Leu Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu	
30 35 40	
gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat	677
Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp	
45 50 55	
cag ccg gct tca caa aaa gct acg tct gaa agc acc gta cag agc	725
Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser	
60 65 70 75	
ggt gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg	773
Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro	
80 85 90	
aag gaa tcg atc caa gat tac gaa cag gaa tat gaa aat cag ctc aaa	821

10295.204.ST25.txt

Lys Glu Ser Ile Gln Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys			
95	100	105	
gac ata ttg gaa acc atc atc ggc gtt gag gac gtg tca atc gtc gtc			869
Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val			
110	115	120	
aat gtt gat gca acc tca ttg aaa ata ttc gag aaa aac aga aaa acc			917
Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr			
125	130	135	
cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg			965
Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr			
140	145	150	155
gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga			
Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly			
160	165	170	
gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg			1061
Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg			
175	180	185	
ggt gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag			1109
Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys			
190	195	200	
acc att att gaa gca gtg aca agg gtt ctt gat gtt ccg agc cac cgc			1157
Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg			
205	210	215	
gtc gct gtt gcc cct aaa aaa atg aag gag gat tca taaatgtatgc			1203
Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser			
220	225	230	
tggaaaaaca aacggtttgg ctttaacca tgttaagtct cgtcggtgtta ctgagtgtct			1263
actacattat gtcgcccggaa ggagaaaatg tcgtcacgggt tgatgacaag gaacaaggttg			1323
ccgctgaaaa agaaaaacccg atgaaaagaag agcctgccaa ggtatggcaaa gatgataccg			1383
cgcctgctaa agacaaaact aaaggaaag atacaaaaga taaagaaaacg tctgcgagtg			1443
agcagaacgg agaggttgtc acagaggaat catcgggtga tgaagattta ttcacaacat			1503
accgcatgga aatggacgat cagcgcagca gggagaggga ggaattaacc gaaatcgta			1563
gaagcgataa agcgacggca aaagaaaaaa gcgaagctta cgacaagatg acagagctca			1623
gcgaagctga aggaacggaa aagacccttg aaaccctcat caaaacaaaa ggcttattaag			1683
acgccttggg caa			1696

<210> 63
<211> 231
<212> PRT
<213> *Bacillus licheniformis*

<400> 63

Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile Gly His Leu Leu Pro
1 5 10 15

Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys Tyr His Tyr Phe Leu
20 25 30

10295.204.ST25.txt

Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu Val Ser Gln Ile Phe
35 40 45

Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp Gln Pro Ala Ala Ser
50 55 60

Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys
65 70 75 80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln
85 90 95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr
100 105 110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr
115 120 125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr
130 135 140

Asn Glu Thr Asp Lys Gln Gly Lys Arg Thr Val Ser Glu Met Ser
145 150 155 160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro
165 170 175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val
180 185 190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala
195 200 205

Val Thr Arg Val Leu Asp Val Pro Ser His Arg Val Ala Val Ala Pro
210 215 220

Lys Lys Met Lys Glu Asp Ser
225 230

<210> 64

<211> 1062

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (498)..(980)

<400> 64
ctacgtctga aagcaccgta cagagcggtg aaggagaaaa agaagtgttc aagccgcct 60
cagatgacaa accgaaggaa tcgatccaag attacgaaca ggaatatgaa aatcagctca 120

10295.204.ST25.txt

aagacatatt ggaaaccatc atcggcggtt aggacgtgtc aatcgtcgtc aatgttgatg	180
caacctcatt gaaaatattc gagaaaaaca gaaaaaccca ggaaacttca acgaatgaga	240
cagataaaca gggaggcaag cggacggtgt ctgaaatgtc ttcagacgaa gaaatcgta	300
tcatcaaaaa cgagataaa gagacgcctg tcgtcggtca gacgaaaaag cccgatatca	360
gggtgttct cgttgcgtc cagggagtgc acaacgttca aataaaaaag accattattg	420
aagcagtgac aagggttctt gatgttccga gccaccgcgt cgctgttgcc cctaaaaaaaa	480
tgaaggagga ttcataa atg atg ctg aaa aaa caa acg gtt tgg ctt tta Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu 1 5 10	530
acc atg tta agt ctc gtc gtt gta ctg agt gtc tac tac att atg tcg Thr Met Leu Ser Leu Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser 15 20 25	578
ccc gaa gga gaa aat gtc gtc acg gtt gat gac aag gaa caa gtt gcc Pro Glu Gly Glu Asn Val Val Thr Val Asp Asp Lys Glu Gln Val Ala 30 35 40	626
gct gaa aaa gaa aaa ccg atg aaa gaa gag cct gcc aag gat goc aaa Ala Glu Lys Glu Lys Pro Met Lys Glu Pro Ala Lys Asp Gly Lys 45 50 55	674
gat gat acc gcg cct gct aaa gac aaa act aaa ggg aaa gat aca aaa Asp Asp Thr Ala Pro Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys 60 65 70 75	722
gat aaa gaa acg tct gcg agt gag cag aac gga gag gtt gtc aca gag Asp Lys Glu Thr Ser Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu 80 85 90	770
gaa tca tcg ggt gat gaa gat tta ttc aca aca tac cgc atg gaa atg Glu Ser Ser Gly Asp Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met 95 100 105	818
gac gat cag cgc agc agg gag agg gag gaa tta acc gaa atc gtc aga Asp Asp Gln Arg Ser Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg 110 115 120	866
agc gat aaa gcg acg gca aaa gaa aaa agc gaa gct tac gac aag atg Ser Asp Lys Ala Thr Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met 125 130 135	914
aca gag ctc agc gaa gct gaa gga acg gaa aag acc ctt gaa acc ctc Thr Glu Leu Ser Glu Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu 140 145 150 155	962
atc aaa aca aaa ggc tat taagacgcct tggtaaacgc cgacggcgat Ile Lys Thr Lys Gly Tyr 160	1010
aaagtcaata ttacggtgaa ggcgaaggag cactcgaaaag ccgcctgcac cg	1062

<210> 65
<211> 161
<212> PRT
<213> *Bacillus licheniformis*

<400> 65

Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu Thr Met Leu Ser Leu
1 5 10 15

10295.204.ST25.txt

val val val Leu Ser Val Tyr Tyr Ile Met Ser Pro Glu Gly Glu Asn
20 25 30

val val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys
35 40 45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro
50 55 60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser
65 70 75 80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp
85 90 95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser
100 105 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr
115 120 125

Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met Thr Glu Leu Ser Glu
130 135 140

Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu Ile Lys Thr Lys Gly
145 150 155 160

Tyr

<210> 66
<211> 3346
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(2843)

<400> 66	gtattcaaaa aacaatttaa cccgtgacat cgagacgaat gtcataggaa aaaatgcggt	60
	taaatacggta ttaatcgatg aaaaccggcg agagacagac aggcgattca aaagctgatg	120
	aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaaa	180
	aaatgccgca gcaaattcgtg ttgcgaggc aggccggaaaa ctcgaactta aaacagatcg	240
	atgtaaacag cgtaccactt ttagtcgaga tgaacggaga ggaagcaagg aacgttcaga	300
	gttctcagca cgaacccgat ggattttta aaacaagaaa cggccctgg gcagacgctt	360
	aaactgacat ttataaata gctggagtgt ctcaaggata aatatgctat aatagggaa	420
	tccagaggaa aatcgcagcc gaaaaaaggc tgctttctt ttgttttac attttttaac	480

10295.204.ST25.txt

acgcagtaag gtgatggAAC atg gca aaa aga aaa cga aaa tca aca aag aaa Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys	533
1 5 10	
caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly	581
15 20 25	
tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta Leu Ile Cys Ile Ala Ile Ser Ile Ala Val Leu Gln Leu Gly Val	629
30 35 40	
gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp	677
45 50 55	
ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe	725
60 65 70 75	
tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt Trp Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu	773
80 85 90	
tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt Tyr Cys Ile Ile Ala Ser Met Leu Leu Ser His Val Gln Leu Phe	821
95 100 105	
cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtc atc caa Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln	869
110 115 120	
aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser	917
125 130 135	
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca Pro Asp Leu Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser	965
140 145 150 155	
tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu	1013
160 165 170	
atc ttg atc ggc ctt ctt ttg att acg gat ccg tcg ctt cag gag acg Ile Leu Ile Gly Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr	1061
175 180 185	
ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp	1109
190 195 200	
cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys	1157
205 210 215	
aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser	1205
220 225 230 235	
gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln	1253
240 245 250	
tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu	1301
255 260 265	

10295.204.ST25.txt

gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu 270 275 280	1349
ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr 285 290 295	1397
ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu 300 305 310 315	1445
ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att Leu Asp Asp Pro Lys His Thr Gly Gln Ala Asp Lys Lys Asn Ile 320 325 330	1493
tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val 335 340 345	1541
aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr 350 355 360	1589
gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu 365 370 375	1637
agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa Ser Asp Asp Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu 380 385 390 395	1685
gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 400 405 410	1733
gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn 415 420 425	1781
gac ccg ccg gat gca aag ctg atg atc ggc ctc ggc ccg aac att tcc Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser 430 435 440	1829
gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val 445 450 455	1877
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475	1925
aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490	1973
att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His 495 500 505	2021
ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gin Ala Leu 510 515 520	2069
aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His 525 530 535	2117

10295.204.ST25.txt

acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met 540 545 550 555	2165
aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val 560 565 570	2213
att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val 575 580 585	2261
gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile 590 595 600	2309
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly 605 610 615	2357
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser 620 625 630 635	2405
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu 640 645 650	2453
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro 655 660 665	2501
ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val 670 675 680	2549
gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met 685 690 695	2597
att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu 700 705 710 715	2645
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val 720 725 730	2693
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745	2741
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly 750 755 760	2789
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu 765 770 775	2837
tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac Ser Ser 780	2893
atctatttat ttatggaca aaacatgata tagttatcct caattaaaga taatttgaat	2953
ctgatctgtc agacggaggg aaaacatgtc gataaaagct gacaatcaac ggttatgttt	3013

10295.204.ST25.txt

aaagggtgatt gatcgataa aagatgatat tcaaatggg gtctttgcg aaaatgaacg	3073
gctcccgagt gaatttgagc tgtcaaagat gcttggtgtg agcagaacgg ctttgcgtga	3133
ggcgcttaga atactggaag aagaaaacgt catcatcaga aggcatggag tcggacattt	3193
tgtaaatgcc agaccgttat ttctatcagg tattgagcag ctgaacagcg tcacaaaaat	3253
gatcgagcag gcaagcatga cgccggAAC cattttatg tcctcacagg ttaccgctcc	3313
cactgaagaa gatatgctcc ggTTTcaata tgc	3346

<210> 67

<211> 781

<212> PRT

<213> *Bacillus licheniformis*

<400> 67

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys			
1	5	10	15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala		
20	25	30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe		
35	40	45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu		
50	55	60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Thr			
65	70	75	80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala		
85	90	95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu		
100	105	110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu		
115	120	125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly		
130	135	140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala			
145	150	155	160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu		
165	170	175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met		
180	185	190

10295.204.ST25.txt

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
450 455 460

10295.204.ST25.txt

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

10295.204.ST25.txt

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780

<210> 68
<211> 1045
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1043)

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		atcaatgaac	ctgtcatttt	cggacttccg	gtcgtgctca	atccaatctt	catgattccc	120								
		tttattatcg	ttccggcagt	caatactgtc	atcggctatt	tgttcatcaa	gtttcagctg	180								
		attccgcccga	tcgcatacgc	tgttccgtgg	acaacgccag	ggccgttgat	tccgttctc	240								
		gggaccggag	gaaaactggct	tgcgtccggc	gtcggctttc	tctgcctcgc	catttcaacg	300								
		atgatttatac	tgccgtttgt	gatggctgcc	aacaagactg	tgaataacgga	cagggagcat	360								
		tccgcggaaa	acaggaaggaa	atcataactt	tagacggggc	gccttttacg	ggcgccccgtc	420								
		ttttttaaa	aaaagtcatg	cggctctctt	ttctctcata	caatctattt	aatcaaaaag	480								
		cacgtctggg	aggaagatatac	atg	cg	aag	ccc	aca	atc	aaa	gag	ctc	atc	ttt	533	
		Met	Arg	Lys	Pro	Thr	Ile	Lys	Glu	Leu	Ile	Phe				
		1						5					10			
caa	cat	atg	aag	gac	cat	ctg	tcg	atc	tat	tta	ttt	gtt	tct	gtg	ctg	581
Gln	His	Met	Lys	Asp	His	Leu	Ser	Ile	Tyr	Leu	Phe	Val	Ser	Val	Leu	
		15						20					25			
ttc	tta	atg	ggt	gtg	att	ttc	ggc	gcf	gtc	atc	gtc	aac	agc	atg	acg	629
Phe	Leu	Met	Gly	Val	Ile	Phe	Gly	Ala	Val	Ile	Val	Asn	Ser	Met	Thr	
		30						35				40				
atc	ggt	caa	aaa	gaa	gat	ttg	ttc	tac	tat	ttg	aat	caa	ttt	ttt	gga	677
Ile	Gly	Gln	Lys	Glu	Asp	Leu	Phe	Tyr	Tyr	Leu	Asn	Gln	Phe	Phe	Gly	
		45						50				55				
cag	ctt	tcc	gaa	gga	aaa	gca	gcc	agc	tca	aag	gaa	atg	ttt	ttg	cag	725
Gln	Leu	Ser	Glu	Gly	Lys	Ala	Ala	Ser	Ser	Lys	Glu	Met	Phe	Leu	Gln	
		60						65			70		75			
agc	ttt	ctt	cat	aat	atg	aaa	tat	tta	ggc	tta	atg	tgg	att	ctc	ggg	773
Ser	Phe	Leu	His	Asn	Met	Lys	Tyr	Leu	Gly	Leu	Met	Trp	Ile	Leu	Gly	
		80							85				90			
ata	tcc	atc	atc	ggt	ctg	ccc	gtc	att	ttt	atc	atg	gtc	ttc	tta	aaa	821
Ile	Ser	Ile	Ile	Gly	Leu	Pro	Val	Ile	Phe	Ile	Met	Val	Phe	Leu	Lys	
		95						100				105				

10295.204.ST25.txt
 ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga 869
 Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly
 110 115 120
 atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att 917
 Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile
 125 130 135
 ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt 965
 Leu Leu Ile Pro Ala Tyr Leu Met Gly Thr Cys Ala Ile Ala Phe
 140 145 150 155
 tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc 1013
 Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser
 160 165 170
 acc tgt cca tgt gtt gtg ccg cggt gta gca gcc ttc aga agc 1045
 Thr Cys Pro Cys Val Val Pro Arg Val Ala
 175 180

<210> 69
<211> 181
<212> PRT
<213> *Bacillus licheniformis*

<400> 69

Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe Gln His Met Lys Asp
 1 5 10 15

His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val
 20 25 30

Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu
 35 40 45

Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly
 50 55 60

Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn
 65 70 75 80

Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly
 85 90 95

Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly
 100 105 110

Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe
 115 120 125

Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala
 130 135 140

Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile
 145 150 155 160

10295.204.ST25.txt

Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val
 165 170 175

Val Pro Arg Val Ala
 180

<210> 70
 <211> 1108
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (500)..(1108)

<400> 70	agtggtcgat gccgtcacga tcacgagcga cacgatttat tacatgctga agcattttgg	60
aagagagatg agagacgaca gtccgtccag gtcgctcgaa cccgcgggaa tgagctttgg	120	
aaaaagaaaag gtcctcaccg aagaagacct tcccgtgaa gagcaccgca aatcgttct	180	
cggtagtc ggaggcctcg cagaggatga aaaaaggcag ctgatccatg aagtccctcg	240	
tccgctcggc cataacttaa tggtgaccctaa taaagaggtc gatacattta tcgatgatat	300	
ggcaaatgtg attgcaaacg gtctgaacac agcgctccat gaaaatgtat cgcaagacaa	360	
taaaggaatg tataaccact aagatcaagg cggctggccc ggccgcgtttt tttcatgaca	420	
tttagcattg ccggaacttg ttctacttcc tctatcttgt acatagtcta ttactagac	480	
aagctctgga gggattttac aat gag aaa aag agg cag gaa tcg tca gtt tgt	532	
Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys		
1 5 10		
gct ggc tgt aaa tgg aag aag cgc ggt tca gac agt att ctt att tat	580	
Ala Gly Cys Lys Trp Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr		
15 20 25		
cgt cag cct gct cgt ttt tat ttt atc agg cgt gct cac atc gct	628	
Arg Gln Pro Ala Ala Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala		
30 35 40		
gcg tcc tca gtt aag gcc gtc ttc atc gtt gta ccg ggt ggc tca tca	676	
Ala Ser Ser Val Lys Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser		
45 50 55		
act gaa ggg cga gac ctt tgg gct cat ttt ggg aat gga aaa cca cta	724	
Thr Glu Gly Arg Asp Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu		
60 65 70 75		
ctt tgc atc aga att gcc gga acc gaa tca gcg ctt tca gct ttc ccc	772	
Leu Cys Ile Arg Ile Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro		
80 85 90		
cct cgt cct gaa gct ggc gac cag cat tca ttt gaa aga tcc gcg aag	820	
Pro Arg Pro Glu Ala Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys		
95 100 105		
ttt tct cgg acg gga gct tcc ggg att ctc tca ttt tca ctc gga aat	868	
Phe Ser Arg Thr Gly Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn		
110 115 120		
cct cat tgc cgg gca agg gac gga tta tac gaa tat gcc gtc aga atc	916	

10295.204.ST25.txt

Pro His Cys Arg Ala Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile	
125 130 135	
tcc gcc gcc gac tca ggt ctt aaa aga gga gag aga agc gaa tct tgc	964
Ser Ala Ala Asp Ser Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys	
140 145 150 155	
aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc	1012
Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser	
160 165 170	
tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca	1060
Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala	
175 180 185	
caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt	1108
Gln Tyr Gly Ile Val Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe	
190 195 200	

<210> 71

<211> 203

<212> PRT

<213> *Bacillus licheniformis*

<400> 71

Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys Ala Gly Cys Lys Trp	
1 5 10 15	

Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr Arg Gln Pro Ala Ala	
20 25 30	

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys	
35 40 45	

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp	
50 55 60	

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile	
65 70 75 80	

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala	
85 90 95	

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly	
100 105 110	

Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala	
115 120 125	

Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser	
130 135 140	

Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu	
145 150 155 160	

Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly	
---	--

10295.204.ST25.txt

165

170

175

Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val
180 185 190

180

185

190

Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
195 200

195

200

<210> 72
<211> 1152
<212> DNA
<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (107)..(985)

<400> 72

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60

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Met Ser Lys
1

115

aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa
Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln
5 10 15

ttt ttt cgt aaa cg_c tgg gta ttt cc_g gcc atc tat ttg aca agt gcc
Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala
20 25 30 35
211

gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac
 Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn
 40 45 50

gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat . . . 307
 Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp
 55 60 65

aac cg^g gat gat gc^g gta gaa gta ggc aaa cca gtc gaa aat gtc gca
 Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala
 70 75 80 355

atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt
 Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe
 85 90 95

gaa	act	gac	gca	act	aaa	gaa	gag	aaa	gaa	gca	gca	ctt	gtc	aac	tat	451
Glu	Thr	Asp	Ala	Thr	Lys	Glu	Glu	Lys	Glu	Ala	Ala	Leu	Val	Asn	Tyr	
100					105				110					115		

aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac 499
 Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp
 120 125 130

gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa
 Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys
 135 140 145

gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa 595
 Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu
 150 155 160

10295.204.ST25.txt

gat ggt tta tca act gtg tat cag tct ctt gaa gta agc gtc aaa Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys 165 170 175	643
caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys 180 185 190 195	691
aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc Asn Leu Tyr Asn Glu Glu Gly Asn His Val His Phe Glu Ile Arg 200 205 210	739
aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val 215 220 225	787
tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu 230 235 240	835
cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala 245 250 255	883
aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser 260 265 270 275	931
tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser 280 285 290	979
cag tca taaggcacgc ttccctcagg gcgcctatca aatgcgatag gcgcctttt Gln Ser	1035
tgttacaatc aaaaaaaaaacc cgtatcaaat cggcggagcc agccgtttt aagtaagagg	1095
cctctttaag gagtggagg cattaggaag taagtagaac agcaaaccgc ctagtaa	1152
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<211> 293	
<212> PRT	
<213> <i>Bacillus licheniformis</i>	
<400> 73	
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Leu Gln Gln Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu 20 25 30	
Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala 35 40 45	
Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser 50 55 60	
Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu 65 70 75 80	

10295.204.ST25.txt

Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys
85 90 95

Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu
100 105 110

Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala
115 120 125

Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr
130 135 140

Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val
145 150 155 160

Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val
165 170 175

Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys
180 185 190

Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Asn His Val His Phe
195 200 205

Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp
210 215 220

Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu
225 230 235 240

Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu
245 250 255

Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg
260 265 270

Glu Asp Ser Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp
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Asp Ser Ser Gln Ser
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<222> (501)..(1244)

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Page 102

10295.204.ST25.txt

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ggcgaaaaa tcatgaagat ccgtcccgtc aacggtgtct ctgcagattt gacgggagcc	180
ctcatcatct ttggcgcgac gatcgccat ttgcctgtca gcacgacaca cgtcatttct	240
tcatccattt taggcgtggg cgcttcccac cgggtgaaag gcgtaaactg gggcaccgca	300
aaggatgc tgatcacttg ggtcattacc cttcccattt cggcaaccat cggtgcattt	360
gcctatttca tacttgattt attctttaa tcagcacact cccgtccgaa tctaggacgg	420
gagttttcat gttaaaaga aagccggcat aacaatagaa ataggaactg cactattct	480
cggaaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu	533
1 5 10	
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15 20 25	
aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu	629
30 35 40	
ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser	677
45 50 55	
att ttc aca aac ccg ctt cat tac ctg atc gtt gcc gtt ttt ttc acg Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr	725
60 65 70 75	
ttg aca gac gct ttt att ttc tta aat gcc tac ttt aaa aag ctc ggc Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly	773
80 85 90	
agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn	821
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gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu	869
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125 130 135	
gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn	965
140 145 150 155	
ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His	1013
160 165 170	
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175 180 185	
cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro	1109
190 195 200	
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10295.204.ST25.txt

Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp			
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Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile			
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tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc			1254
Tyr Asp Leu Leu Leu Pro Asn Glu Glu Gly Asp Asp			
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gcaatccaaa accaatatcg cgaaatacga agtcagcccc tataccgaac ggattttccg			1374
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aaattctccc gtccttattc cgtttcccg tttcttacat acaataaacc aatcaactaa			1494
accgctaat taggtgatgc tgtgaaaaaa ctgaaaaaac aagtcaaaca cgtcgatttc			1554
gcaaaattcg gcctgtcaga ctatacctct cttctcagaa gaagaagcga aaaaatcatt			1614
aaaacgctga acagaagaaa aaacaaaccg tgaagcttgg actttcaccc tccttctctg			1674
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<210> 75

<211> 248

<212> PRT

<213> *Bacillus licheniformis*

<400> 75

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Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly		
35	40	45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro		
50	55	60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe			
65	70	75	80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala		
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Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr		
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Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro		
115	120	125

10295.204.ST25.txt

Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr Ala Glu Gly Ile Glu
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Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn Ile Ser Ala Ala Leu
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Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His Leu Leu Glu His Met
 165 170 175

Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp Arg Lys Asp Val Tyr
 180 185 190

Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro Phe Ser Ile His Asp
 195 200 205

Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp Leu Val Thr Glu Phe
 210 215 220

Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile Tyr Asp Leu Leu Leu
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Pro Asn Glu Glu Glu Gly Asp Asp
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<210> 76
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 <212> DNA
 <213> *Bacillus licheniformis*

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tattatttca gaagagattt taaaagagga aatggaaat ttacgagagg aagaaaaattt	240
aataataact cgaattgaaa aattacagca cctcattaaa ctcagagata aaaccttttt	300
aaccaatatac atttcaactt cactacacga tctaaagaac ttttcaata ttatcgaaaga	360
tgtgacaaa aaggaattac ttcgttctct cattgaagag attcacgtaa atccaggaaa	420
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atcaattgaa ctaagagaag gggAACATCT tttctctttt ttgtgtttca tattataatt	533
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Met His Ile Lys Arg Val Ala Ile Tyr Cys	
1 5 10	
aga gtt tct acc gaa gag cag gca acg gaa tac agc ata tct gcc	581
Arg Val Ser Thr Glu Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala	
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10295.204.ST25.txt

caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att Gln Leu Gln Thr Leu Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile 30 35 40	629
gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly 45 50 55	677
cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe 60 65 70 75	725
caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu 80 85 90	773
gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc Asp Thr Leu Thr Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe 95 100 105	821
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gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu 125 130 135	917
tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser 140 145 150 155	965
tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu 160 165 170	1013
gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu 175 180 185	1061
tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys 190 195 200	1109
gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val 205 210 215	1157
gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu 220 225 230 235	1205
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cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu 255 260 265	1301
tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg 270 275 280	1349
caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp 285 290 295	1397

10295.204.ST25.txt

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gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn 320 325 330	1493
aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala 335 340 345	1541
gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn 350 355 360	1589
cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser 365 370 375	1637
tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca Leu Asn Gln Leu Asn Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser 380 385 390 395	1685
gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg 400 405 410	1733
cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga Pro Tyr Gln	1782
aaaagcagag ttagaacaaa ggcacaatga atcaactggc aattaagctc gaacgatgca aaagtaataa aaccagaact gattcaaaaag cttagaaaa aattccttta gtctataaac atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcattatt	1842 1902 1962 2020

<210> 77
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<212> PRT
<213> *Bacillus licheniformis*

<400> 77

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20 25 30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val
35 40 45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln
50 55 60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val
65 70 75 80

10295.204.ST25.txt

Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Leu
85 90 95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu
100 105 110

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met
115 120 125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys
130 135 140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val
145 150 155 160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys
165 170 175

Glu Ala Glu Ile Val Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys
180 185 190

Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr
195 200 205

Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp
210 215 220

Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp
225 230 235 240

Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu
245 250 255

Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln
260 265 270

Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro
275 280 285

Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met
290 295 300

Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys
305 310 315 320

Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala
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Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile
340 345 350

10295.204.ST25.txt

Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn Gln Leu Phe Ser Lys
 355 360 365

Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser Leu Asn Gln Leu Asn
 370 375 380

Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser Glu Ile Gln Glu Tyr
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Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg Pro Tyr Gln
 405 410

<210> 78
<211> 1417
<212> DNA
<213> *Bacillus licheniformis*

<220>
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<222> (510)..(1298)

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	cgtatccatcc cgacgtatcc cagctgaaag cgagtcgatg cggcgcata agctcgatca	180
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	ggaaatcatt aggataaac caggcggcga tgccttcact ggtggcgacg gcctcccaca	300
	ctttttctat cgatgcgtga aaaacagcct gtttatgtat atcaggcact agttgattgc	360
	tcataataga cctcctagaa aaaagtaaaa ccaaattgtt tcctttctat tatatgaaac	420
	cttttagttt tatgtcaatg ttccgtcata attccctggg acaaggcata tcattgaaca	480
	aacgaacctg aatgtaaagg atgagggtt atg agt cat aga gca gat gag att	533
	Met Ser His Arg Ala Asp Glu Ile	
	1 5	
	cga aaa aga atg gcc agg aaa aga aag cgg aaa aca ccg gac aaa cag	581
	Arg Lys Arg Met Ala Arg Lys Arg Lys Lys Thr Pro Asp Lys Gln	
	10 15 20	
	ccc ttt tca tca gac ggc aaa aag cgg ccg ctc aag ccg cct gca tgg	629
	Pro Phe Ser Ser Asp Gly Lys Lys Arg Pro Leu Lys Pro Pro Ala Trp	
	25 30 35 40	
	aca gcc ttt tcg gaa gat gaa aaa gga gga gac ttc cct ccg cct gaa	677
	Thr Ala Phe Ser Glu Asp Glu Gly Gly Asp Phe Pro Pro Pro Glu	
	45 50 55	
	gga agt tcc ctg ctg ata aac ggg aag cac ccg ctt gtc aag gcg gat	725
	Gly Ser Ser Leu Leu Ile Asn Gly Lys His Pro Leu Val Lys Ala Asp	
	60 65 70	
	gcg ctc atc ttg aaa tgt ctt ctg tcg gca tgc ctt gtt ctt gtg tcc	773
	Ala Leu Ile Leu Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser	
	75 80 85	
	gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg	821

10295.204.ST25.txt

Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro
 90 95 100

gta atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag 869
 Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln
 105 110 115 120

aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg 917
 Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro
 125 130 135

aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct 965
 Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala
 140 145 150

gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag ggc att 1013
 Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile
 155 160 165

aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat 1061
 Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr
 170 175 180

gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg 1109
 Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu
 185 190 195 200

cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg 1157
 Gln His Ala Asp Asn Ser Tyr Thr Tyr Gly Gln Leu Lys Lys Ala
 205 210 215

gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg 1205
 Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr
 220 225 230

att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa 1253
 Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys
 235 240 245

caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag 1298
 Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu
 250 255 260

taaatggacg gagctttca ccaagttca cattcatccg ctgctgtggc ttgtcatggc 1358

gatcggtatc atgacaggac atattaaagg cgcgtttt gtttaatgca cccaggaag 1417

<210> 79
 <211> 263
 <212> PRT
 <213> *Bacillus licheniformis*
 <400> 79

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Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys
 20 25 30

Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys
 35 40 45

Gly Gly Asp Phe Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly
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10295.204.ST25.txt

50

55

60

Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu
 65 70 75 80

Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe
 85 90 95

Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu
 100 105 110

Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly
 115 120 125

Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln
 130 135 140

Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln
 145 150 155 160

Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr
 165 170 175

Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro
 180 185 190

Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr
 195 200 205

Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile
 210 215 220

Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys
 225 230 235 240

Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro
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Ile Gln Val Ile Thr Phe Glu
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<210> 80

<211> 1468

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (982)..(1428)

<400> 80

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GCTGCTCTG TTCGTCGGTG CGGGCCTTGC CGTCATGAAC TTTCATGAAG ATGTCAGCAT	300
GAGGGAAGTG CACATCCTGC TTTACGAAAT GGTGACGGGC AAGGTGAACC GCTATCCATA	360
CCTTTGCAG GTTCCGTACA GCATCGGTCT TGGCCTCGGC ATGATCTTGT TTTTAATCA	420
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TCAGCTTGAT TTGGACCATT ATGTGGCCAT GCACGAAAAC AAAGAAAACGA CAAAGGATAT	540
TCATGATCAT TAGCGTATAA TTTATCATCT TTCTCGGACT CGCAGGAGGG GTTGCTGTTG	600
GATCCGGCTT TGTGCTTTT CTTACCGTGC TTGGCATTAT CCCGAGGCTG ACTCAGCTGA	660
CGAAAACAAA AGGATTTATC CAGGCGTATG AATGGGCTGT CATTAGGC GCGGTTTCG	720
GAGGATGGGA ATCGCTGAAC ATGTCCCCT TTTTTTATC CAAATGGCTG CTTGTTCCGA	780
TCGGCCTTT TGCAGGCGTT TTCATTGAA TGCTTGAGC GGCAGCTAACAA GAAGTCTTGA	840
ACGTGCTGCC GATACTGGCG AAACGCACTCG GGATGGGAGA CCAGGATTTG ATACTTTAA	900
TGGCCATTGT TTTCGGCAAG ATTCTCGGAT CGATGTTCCA ATGGCTCATT TTTGTTCAATT	960
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AAA GTT AAA GCG TAT CAG CCT TCA CCG CCT TAT GTC CTG AAC TGT ATC Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile 15 20 25	1059
AAG GCA TTT CTC GTC GGT GGT CTG ATT TGT ACG ATC GGC CAG GCT TTC Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe 30 35 40	1107
CAG AAT TTT TAT ATG GCT GTG TTC CAT TTT GAT GAA AAA ACG GCC GGG Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly 45 50 55	1155
AAC CCG ACG GTT GCC ACG CTG ATC CTG ATC TCC GCT CTG TTA ACA GGC Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly 60 65 70	1203
CTT GGC GTC TAC GAC AGA ATC GGA CAG TTT GCC GGC GCT GGT TCT GCC Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala 75 80 85 90	1251
GTT CCG GTC ACA GGG TTT GCC AAC AGT ATG ACG AGC GCA GCG CTG GAG Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu 95 100 105	1299
CAT AAA AGC GAA AGC TAC GTC CTC GGC GTC TGG ACA AAC ATG TTC AAG His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys 110 115 120	1347
CTT GCG GGA AAC GTC ATC GTG TTC GGT GTC GGC GCT TAT ATT GTG Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val 125 130 135	1395
GGG ATG ATC CGC TTT GCC TTT GAC AAG CTG TTT TAGGAGAAA ACATCATGAA Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe	1448

10295.204.ST25.txt

140

- 145

1468

at taacagga aaacaaacat

<210> 81
 <211> 149
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 81

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
 1 5 10 15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
 20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
 130 135 140

Phe Asp Lys Leu Phe
 145

<210> 82
 <211> 1453
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (504)..(950)

<400> 82
 ttcggatcc ttatgtggcc atgcacgaaa acaaagaaac gacaaaggat 60
 attcatgatc attagcgtga tatttatcat ctttctcgga ctcgcaggag gggttgtgt 120
 tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccggagc tgactcagct 180

10295.204.ST25.txt

gacgaaaaca aaaggattta tccaggcgta tgaatgggct gtcattttag gcgcggttt	240
cgaggatgg gaatcgctga acatgtcccgttttttta tccaaatggc tgcttgtcc	300
gatcggcctt ttgcggcgcttgcattgg aatgcttgcgcggcgctaa cagaagtctt	360
gaacgtgctg ccgatactgg cgaaacgcat cggatggga gaccggatttgataactttt	420
aatggccatt gtttcggca agattctcgatcgatgttc caatggctca ttttgttca	480
tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser 1 5 10	533
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile 15 20 25	581
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe 30 35 40	629
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly 45 50 55	677
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly 60 65 70	725
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala 75 80 85 90	773
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu 95 100 105	821
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys 110 115 120	869
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val 125 130 135	917
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe 140 145	970
attAACAGGA AAACAAACAT GGAAATTGCA GAACCGCTG TTTGTTAACT CAAGCGGAAC AGCGGTCGGT CCCAAAGAAA AAGAAGGTCC TCTTGGACAC TTATTTGACA AAAGCTATGA TGAAATGCAC TGCAACCAGA AAAACTGGGA AATGGCAGAG CGCAAGCTGA TGGAGGATGC GGTCAGTCC GCGTTATCAA AACAAATCT TAAAAAGGAA GACATCGATA TCTTTTGGC TGGCGATCTG CTCAACCAAA ACGTGACAGC CAACTATGTG GCGCGGCATT TGAAAATTCC TTTTCTCTGC TTATTTGGAG CATGCTCGAC ATCAATGGAA TCAGTCGCGA TCAGTTGGC GTTGATTGAC GGGGGTTTCG CAAAGCGCGC CCTAGCGCA ACCAGCAGCC ATAATGCTAC GGCAGAAAGG CAGTTCCGCT ACCCGACGGA ATACGGGGGG CAAAACCGG GAACCGCGAC TTT	1030 1090 1150 1210 1270 1330 1390 1450 1453

10295.204.ST25.txt

<210> 83
<211> 149
<212> PRT
<213> *Bacillus licheniformis*

<400> 83

Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1 5 10 15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
130 135 140

Phe Asp Lys Leu Phe
145

<210> 84
<211> 2020
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1517)

<400> 84	gctcattttt gtcatttgt cataaaagga ggattatgtat gtcaagtttg aaagataatt	60
	atcaatcgaa agttaaagcg tatcagcctt caccgcctta tgtcctgaac tgtatcaagg	120
	catttctcgt cggtggtctg atttgtacga tcggccaggc tttccagaat ttttatatgg	180
	ctgtgttcca ttttgatgaa aaaacggccg ggaacccgac gtttgccacg ctgatcctga	240

10295.204.ST25.txt

tctccgctct gttaacaggc cttggcgatct acgacagaat cgacatgtt gcccggcgctg	300
gttctgccgt tccggttaca gggttgccca acagtatgac gagcgcagcg ctggagcata	360
aaagcgaaag ctacgtccctc ggcgtatgga caaacatgtt caagcttgcg ggaaacgtca	420
tcgtgttcgg tggtgtggcc gcttatattg tggggatgat ccgcttgcc tttgacaagg	480
tgtttagga ggaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe	533
1 5 10	
gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys	581
15 20 25	
gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu	629
30 35 40	
atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met	677
45 50 55	
gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu	725
60 65 70 75	
gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr	773
80 85 90	
gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe	821
95 100 105	
gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu	869
110 115 120	
att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His	917
125 130 135	
aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly	965
140 145 150 155	
caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val	1013
160 165 170	
gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val	1061
175 180 185	
gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser	1109
190 195 200	
gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat Ala Met Ala Pro Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp	1157
205 210 215	
ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu	1205
220 225 230 235	

10295.204.ST25.txt

tca ggc gtc ggc agc ccg att ttg aag gat ctg tta aaa gag gaa gga Ser Gly Val Gly Ser Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly 240 245 250	1253
atc aat gtc ggg aca aaa cat aat gac tgc ggg ctg atg atc tat acg Ile Asn Val Gly Thr Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr 255 260 265	1301
cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala 270 275 280	1349
gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu 285 290 295	1397
aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc Asn Arg Val Leu Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile 300 305 310 315	1445
atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe 320 325 330	1493
gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcatttgc cttttattgc Glu Arg Ala Glu Arg Gly Asn Ala 335	1547
aggcgggctg atttgcgtca tcggacagct cttgcttgat atcttcaaaa tgacgccggc tcatgtcatg tcaacttttgcgttatctgg agcgatcctt gacggattcg gcatttacga ccgtttatc gaatttgcgttatctggccgc tacagtccccg attgtcagct tcggccactc tctttgcac ggcgcgatgc accaggctga gaaacatggc tttatcgaa tcggcatggg gatatttgcgttatctggccgc tacagtccccg attgtcagct tcggccactc ctgatattttttt aaaccgaaag gataaaggaa aatgccagca aaacgcagg tcattttgtgc cacagacggc gatatacgt ctgaaaagc aatcgaatat gcagcaagaa aaacgggtgg ccgctgcatt tcccaatcgg cggggaatcc gagcgttaaa acaggaccgg agc	1607 1667 1727 1787 1847 1907 1967 2020

<210> 85
<211> 339
<212> PRT
<213> *Bacillus licheniformis*

<400> 85

Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe Glu Asn Pro Leu Phe
1 5 10 15

Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro
20 25 30

Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln
35 40 45

Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln
50 55 60

10295.204.ST25.txt

Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe
65 70 75 80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala
85 90 95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr
100 105 110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe
115 120 125

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu
130 135 140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr
145 150 155 160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln
165 170 175

Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp
180 185 190

Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala
195 200 205

Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro
210 215 220

Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser
225 230 235 240

Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr
245 250 255

Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val
260 265 270

Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala
275 280 285

His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val
290 295 300

Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu
305 310 315 320

Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg
325 330 335

10295.204.ST25.txt

Gly Asn Ala

<210> 86
<211> 2473
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1970)

<400> 86	cgaatatgca gcaagaaaaa cgggtggccg ctgcatttcc caatcgccgg ggaatccgag	60	
	cgtaaaaaca ggaccggagc ttgttaaccat gatcctgcaa acccctcatg atcctgtatt	120	
	cgtcatgtt gatgattccg gacttcaagg tgaaggcccgg gagagacag ctagaaata	180	
	tgtagcgatg catccccata tcgaggtgct cggagtcatc gccgtcgctt caaaaactca	240	
	ttatgcagag tggacgagag tcgatgtatc aatcgatgca gaaggcgaac tgacagagta	300	
	cggcgtcgat aaacacgggg tcaaagagtt cgatgtcaaa cgaatgaatg gtgatacagt	360	
	ctattgcctt gaccagctgg atgttccgat cattgtcgga atcggtgata tcggtaagat	420	
	gaacagaaaaa gacgatgtgg aaaaagggttc gccgattaca atgaaagcgg tcgagctcat	480	
	tttagaaagg agcgggtatc atg agt gct caa aag' caa gag aag acg aac gta	533	
	Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val		
1	5	10	
	ttc ctt gat cct tct aag aat gaa gcg tat ttc aag aag cgg gtc ggc	581	
Phe Leu Asp Pro Ser Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly			
15	20	25	
atg gga gaa agc ttt gac ctt ggc gta cgg aag gtc ttt att ctc gga	629		
Met Gly Ser Phe Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly			
30	35	40	
cat gaa gtt cag ctt tat tat gtc aac gga ttg tgc gac aca caa tac	677		
His Glu Val Gln Leu Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr			
45	50	55	
atc att cac ctg tta aga gaa ctg gtg cat ctg aat gat aaa gaa aaa	725		
Ile Ile His Leu Leu Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys			
60	65	70	75
gaa tcg ggc gag gtc gaa gac atc gtc gaa aac agg ctt ttg aac cag	773		
Glu Ser Gly Glu Val Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln			
80	85	90	
cag gtt tca aaa gcg gaa acg ctt gat gaa gct gtc gac caa gtg ttg	821		
Gln Val Ser Lys Ala Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu			
95	100	105	
tca gga ctg gtt gcc atc atc gtc gaa gat gcg ggc ttt gct ttt atc	869		
Ser Gly Leu Val Ala Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile			
110	115	120	
atc gat gtc aga agc tac ccg ggc aga acg ccg gaa gaa cct gat aca	917		
Ile Asp Val Arg Ser Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr			
125	130	135	
gaa aaa gtc gta cgc ggt gca agg gac gga ctc gtc gag aac atc atc	965		

10295.204.ST25.txt

Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile	155	
140 145 150		
gtc aac aca gcc ctg att aga cgc cg ^g atc aga gat gag cgc ttg cgc	1013	
Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg		
160 165 170		
tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc	1061	
Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu		
175 180 185		
tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa	1109	
Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys		
190 195 200		
aaa gaa att gaa gat g ^t g aag atc gac ggg ctg ccg atg tcg gat aaa	1157	
Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys		
205 210 215		
tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt	1205	
Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu		
220 225 230 235		
gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag	1253	
Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu		
240 245 250		
ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca	1301	
Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr		
255 260 265		
ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag	1349	
Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Tyr Arg Gln		
270 275 280		
acg ccg gct gtt ggg acg ttt tta agg tgg gtg ccg ttt ttc ggt att	1397	
Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile		
285 290 295		
ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat	1445	
Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His		
300 305 310 315		
ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac	1493	
Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp		
320 325 330		
acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc	1541	
Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val		
335 340 345		
gaa ttt tta aga atg gcc g ^c c att cat acg ccg acg g ^c g ctt tcg act	1589	
Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr		
350 355 360		
gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc g ^c g atc aat	1637	
Ala Met Gly Leu Ile Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn		
365 370 375		
gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca	1685	
Val Gly Leu Phe Ser Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala		
380 385 390 395		
atc gga gcc tac acg aca cca agc tac gag ctg agc ctg g ^c g aat aaa	1733	
Ile Gly Ala Tyr Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys		
400 405 410		
atg gtg aag ctg ttt atg ctg ata ttg gtg g ^c g ctt ttt aaa gtg gag	1781	

10295.204.ST25.txt

Met Val Lys Leu Phe Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu			
415	420	425	
gga ttt gtc atc gga tta acg atc tta act ata gtg atg act tcg atc			1829
Gly Phe Val Ile Gly Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile			
430	435	440	
agg tca ttg cga acg cct tac tta tgg cct ctc ctc ccg ttc aat gga			1877
Arg Ser Leu Arg Thr Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly			
445	450	455	
aaa gcg ttt tgg cat gtt ctc gtg cgc acg tcc gtt cca ggg gga aaa			1925
Lys Ala Phe Trp His Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys			
460	465	470	475
gtc agg ccg agc atc gtt cat ccg aga aac cgc tcc aga cag ccg			1970
Val Arg Pro Ser Ile Val His Pro Arg Asn Arg Ser Arg Gln Pro			
480	485	490	
tgaagccggc attcgaagag gcttttcccc ggggaaaagc ctcttttca ataatcgaaat			2030
tccggtcttt gagtaccgat gcctctgtat tcattggcag agatcgac tgcccgagg			2090
ctgcagatgt tgttctgtct tctgatcgga tagacgacat acagcatttc gcggccgtac			2150
gggtcaatcg ttgacgaatg aaggaaaacc tcagttccctc tccgccaaaa tctcgattc			2210
gccggagctg taataatctg cccttcataaa ggctcataaa ttctctgttc ataatgcgca			2270
gccggctgat aaggggcgta tacatctca ggtcatagc cgggagcggg ggtgttaggga			2330
taacgatttg gatacatatg ataacctt tcccacttcg tttttgggtt ttcatctta			2390
agattatatt caggtaaatg cctatttcta tggcgaaaa tctcagcttt tcggctctt			2450
ttttattgaa tggacgttgt gta			2473

<210> 87
<211> 490
<212> PRT
<213> *Bacillus licheniformis*

<400> 87

Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val Phe Leu Asp Pro Ser
1 5 10 15

Lys Asn Glu Ala Tyr Phe Lys Arg Val Gly Met Gly Glu Ser Phe
20 25 30

Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu
35 40 45

Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu
50 55 60

Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val
65 70 75 80

Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala
85 90 95

10295.204.ST25.txt

Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala
100 105 110

Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser
115 120 125

Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg
130 135 140

Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu
145 150 155 160

Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His
165 170 175

Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp
180 185 190

Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp
195 200 205

Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe
210 215 220

Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu
225 230 235 240

Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val
245 250 255

Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr Pro Thr Thr Leu Phe
260 265 270

His His Val Gln His Ala Glu Glu Tyr Arg Gln Thr Pro Ala Val Gly
275 280 285

Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile Leu Ala Ser Thr Phe
290 295 300

Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His Pro Ser Leu Leu Pro
305 310 315 320

Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp Thr His Ile Pro Ile
325 330 335

Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val Glu Phe Leu Arg Met
340 345 350

Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr Ala Met Gly Leu Ile
355 360 365

10295.204.ST25.txt

Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn Val Gly Leu Phe Ser
370 375 380

Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala Ile Gly Ala Tyr Thr
385 390 395 400

Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys Met Val Lys Leu Phe
405 410 415

Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu Gly Phe Val Ile Gly
420 425 430

Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile Arg Ser Leu Arg Thr
435 440 445

Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly Lys Ala Phe Trp His
450 455 460

val Leu val Arg Thr Ser Val Pro Gly Gly Lys Val Arg Pro Ser Ile
465 470 475 480

Val His Pro Arg Asn Arg Ser Arg Gln Pro
485 490

<210> 88
<211> 1567
<212> DNA
<213> *Bacillus licheniformis*

<220>
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<222> (501)..(1064)

<400> 88
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 cagccgcttt acgagctgac tgtcacagca aagccgaaga acattccgca gacgatcgag 180
 gttgatattt ccagtctcgat agtcaatgat gttctaaccg tcggcgatat tccgacc 240
 ggcgattatt catacaacca tgaggctgat gaagttttg catccattct tcctcctcaa 300
 aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc 360
 actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt 420
 tgtgcttagaa tgaggggaaa tttaggatgct cccccctcagt atgctgaggc agggtttgc 480
 ttaagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt 533
 Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly
 1 5 10
 aaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac 581
 Lys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp
 15 20 25

10295.204.ST25.txt

gag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac Glu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn 30 35 40	629
gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val 45 50 55	677
aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu 60 65 70 75	725
ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp 80 85 90	773
gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser 95 100 105	821
gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca Ala Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr 110 115 120	869
agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly 125 130 135	917
atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu 140 145 150 155	965
ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala 160 165 170	1013
tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys 175 180 185	1061
gta taaggcaaaa gggAACGGAA catactagtc ttAAAAAGAC tcggtatgga Val	1114
ggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cgaaagtctt	1174
gaccattctt atgtaaacag tgaacagtta ggcttaacc acttaacaaa tgatgaaaga	1234
aacgatatga ttcttatat ggataatggg gatcacacg tgaagacgat atgtgaagat	1294
tgtcaagaag cgcttgagcg aaaccggat tatcaccaat atcattcatt tattcaatag	1354
atagctttgg ttagagact agaccaaagc attttctat ttgaggaaga gaggaggggc	1414
tcatttgaac aatattcaat cctatataac aaaaagcgat gattttaaat ccatcgtaa	1474
cggcttgaac gaagggtctga aggaacagct gcttgcgggg ctctccggat ctgccccgtc	1534
gttatttaca gccgcttta caaaagaaac gag	1567

<210> 89
<211> 188
<212> PRT
<213> *Bacillus licheniformis*
<400> 89

10295.204.ST25.txt

Met Leu Val Phe Ala Gly Leu-Gly Asn Pro Gly Lys Thr Tyr Glu Asn
 1 5 10 15

Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu
 20 25 30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile
 35 40 45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr
 50 55 60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu
 65 70 75 80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro
 85 90 95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn
 100 105 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg
 115 120 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp
 130 135 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu
 145 150 155 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro
 165 170 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val
 180 185

<210> 90
 <211> 2097
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1598)

<400> 90
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 aaacagactg ttttacaatg acagcaaagc gacaaacatt cttgcacga aaaaagcgct 120
 gtccgcctt caaaagccgg tcattttgct ggcagggggg cttgaccgcg gaaatgaatt 180
 tcatgtacta aagccgcata tgtctttgt aaaagcggtg atcactttcg gcgagaccgc 240
 gcccgaagttt gagaagctgg ccgaagaaat ggaaatacaa caggttaaac gtgtcgataa 300

10295.204.ST25.txt

tgttgaacaa gcagcaactg cggcgttcag cctgtcagac gaaggagatg tcattttct	360
gtccccggcc tgcgcaagct gggatcagta caaacattt gaagaacgtg gtgacatgtt	420
tgtaaacgcc gtgcataatgc taaaataagg gcttgtctcg taaagatagc cctaagaatt	480
agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu	533
1 5 10	
ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta Leu Val Ile Ile Thr Leu Leu Leu Thr Ile Gly Leu Ile Met Val	581
15 20 25	
tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe	629
30 35 40	
ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala	677
45 50 55	
atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala	725
60 65 70 75	
aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val	773
80 85 90	
ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val	821
95 100 105	
ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile	869
110 115 120	
gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser	917
125 130 135	
ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe	965
140 145 150 155	
ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val	1013
160 165 170	
ggc aca tgc att att atg atc ttt gtc gcg ggg gcg aga att tcg cac Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His	1061
175 180 185	
ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val	1109
190 195 200	
ctg tcg gcg ccg tac cgg atc aaa agg atc act tca tac ttg aac cct Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro	1157
205 210 215	
tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr	1205
220 225 230 235	
gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc gac agc agg	1253

10295.204.ST25.txt

Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
 240 245 250
 Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
 255 260 265
 1301
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 Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
 270 275 280
 1349
 ctc ttc agc gtt cta tta tgg aga ggc atc aga atc gcg ctc ggt gcg
 Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
 285 290 295
 1397
 ccc gat tta tac ggc agt ttt gtc gcc gtc ggc gtc att tcg atg ata
 Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
 300 305 310 315
 1445
 gcg att cag gtt atg atc aat atc gga gtc gtg act ggt ttg att cct
 Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
 320 325 330
 1493
 gtt aca ggc att acg ctt ccg ttt tta agc tat ggc ggt tca tca ctg
 Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
 335 340 345
 1541
 acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg aat gtc agc agg tat
 Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
 350 355 360
 1589
 tct aga tac tagattttgg cgataaccct gttgcgagat agcagggtta
 Ser Arg Tyr
 365
 1638
 tcggcggtta cataaggatt aagggggaga acagatgcgg attgttgtta gcggaggcgg
 1698
 aacggggcgc catatttacc ccgccttgc gtttattaaa gaagtgaaac ggcacacgca
 1758
 agatgttgag ttttatata tcgaaaccga aaaaggcctg gagaaaaata tcgtcgagcg
 1818
 ggaagggatc ctttcaaag cgattgaaat tacgggttt aaaagaaaac tttcatttga
 1878
 aaacgtcaaa accgtcatgc gcttttaaa gggtgtaaaa gaatgcaaag aagaattaaa
 1938
 acggttcaag ccggatgccg tgatccgcac gggcggctac gtgtcggcc ccgtcgata
 1998
 cgccgcttca aaactgggaa ttccgacgat tatccacgaa caaaacagcc ttcccggact
 2058
 caccaataag ttttatcca aatatgttga taaggttagc
 2097

<210> 91
 <211> 366
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 91

Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu Leu Val Ile Ile Thr
 1 5 10 15

Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val Tyr Ser Ala Ser Ala
 20 25 30

Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg
 Page 127

35

40 10295.204.ST25.txt
45

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met
50 55 60

Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile
65 70 75 80

Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met
85 90 95

Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile
100 105 110

Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys
115 120 125

Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe
130 135 140

Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met
145 150 155 160

Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile
165 170 175

Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly
180 185 190

Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr
195 200 205

Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu
210 215 220

Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly
225 230 235 240

Gly Leu Phe Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr
245 250 255

Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu
260 265 270

Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Phe Ser Val Leu
275 280 285

Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly
290 295 300

Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met
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305

310

10295.204.ST25.txt

315

320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr
 325 330 335

Leu Pro Phe Leu Ser Tyr Gly Ser Ser Leu Thr Leu Met Leu Met
 340 345 350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr
 355 360 365

<210> 92
 <211> 1882
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1397)

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	aaaagaaatc gttgatgtta agcgggccga acggctcggc gtactgggc agacggacct	180	
	tgagatcaat gaggcaggacg gtcagattac cgctcttatac atcccttctg ttaaatggtt	240	
	cggacttagga agaaaacagg ggaatgacat taaggtgccc tggtcgcaaa ttcaaaaaat	300	
	cggctcggat atgatcattt tggatgttcc ggaaagcagc gtgacaaggaggtaagc	360	
	aaggtggaaa cccgccccgtc ccatgggggc gggcttttg ttttctgga tttcaattca	420	
	ccgctatttc ctttttgtca tatgatgaaa ttagcttatg aattagatcc ttgtcaaaaa	480	
	agaaggtgaa tggtagagcc atg tta acc gga ttg acg att gca atc atc ggc	533	
	Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly		
1	5	10	
	ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat	581	
Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp			
15	20	25	
gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc	629		
Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr			
30	35	40	
gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac	677		
Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp			
45	50	55	
agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg	725		
Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala			
60	65	70	75
act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa	773		
Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu			
80	85	90	
aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat	821		
Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr			

95	100	105		
tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe 110 115 120			869	
gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly 125 130 135			917	
gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser 140 145 150 155			965	
aat gta atg gtt ctc ggg ctg ggg cg ^g acg gga atg agc atc agc cgg Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg 160 165 170			1013	
acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser 175 180 185			1061	
gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr 190 195 200			1109	
aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr 205 210 215			1157	
att cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc Ile Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro 220 225 230 235			1205	
aga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt Arg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe 240 245 250			1253	
gat ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt Asp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu 255 260 265			1301	
ccc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt Pro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val 270 275 280			1349	
ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser 285 290 295			1397	
taatgtcgat caaaggaaaa agaattcgat ttggcctaac gggtcacat tgtacgtatg atgccgttt tcccgagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggctcg tgacgcatac tgtcaagtgc acggatacac gctttggaga agggaaagaa tgggtcagaa gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg ggccgaaaac accgctggac tgcatggtg ttgcgccatt gacggaaat tcgatgagca agcttgc ^a aaa cggccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa actcccgatcc cgtcgatcc ggcatttcaa cgaatgacgc gctcggcttg aacggcgtca acttgcgatgag gctgatggcg gcaaaaaatg tttactttat tccgatccggc caggatgacc cttac				
				1457
				1517
				1577
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				1757
				1817
				1877
				1882

10295.204.ST25.txt

<210> 93
<211> 299
<212> PRT
<213> *Bacillus licheniformis*

<400> 93

Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly Gly Asp Ala Arg Gln
1 5 10 15

Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp Ala Lys Val Phe Leu
20 25 30

Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu
35 40 45

Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro
50 55 60

Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn
65 70 75 80

Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His
85 90 95

Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala
100 105 110

Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile
115 120 125

Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala
130 135 140

Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu
145 150 155 160

Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu
165 170 175

Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg
180 185 190

Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu
195 200 205

His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile
210 215 220

Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu
225 230 235 240

10295.204.ST25.txt
 Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Ala Glu Lys
 245 250 255

Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala
 260 265 270

Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu
 275 280 285

Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
 290 295

<210> 94
 <211> 1588
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1088)

<400> 94 atacctacag tcgaagggtgc cattatgatg gccatacagc atacagactt tacgattcac ggctcgaaatg taatggttct cgggctgggg cggacgggaa tgagcatcag ccggacgttc tcggcgctcg ggcacgcgt aaaagtccga gctcgact ccccccaccc cggccagaatc atggagatgg gcctcactcc tttccacaca aacgaacttg cagagcatgt tgaaaatatc gacatatgca tcaataccat tccaaggctg attctcgata aacatgtcct ctcacgaatg acacccagaa cattaattct cgatttagca acccgccccg gaggcacaga ttttgatttt gccgaaaagc aaggcattaa agcgctgctt gctccaggac ttcccccggat cgtcgcgcct aaaacggcgg gacagatcat tgccaatgtt ttgtgcaacc ttttgtctga attaacaact gaccgaaagg ggctgtcata atg tcg atc aaa gga aaa aga atc gga ttt ggc Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly 1 5 10	60 120 180 240 300 360 420 480 533
cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu 15 20 25	581
gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr 30 35 40	629
gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg 45 50 55	677
aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys 60 65 70 75	725
gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala 80 85 90	773
cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac	821

10295.204.ST25.txt

Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp	95	100	105	
agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc				869
Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro				
110		115		120
gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc				917
Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val				
125		130		135
aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc				965
Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe				
140		145		150
ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg				1013
Gly Gln Asp Asp Pro Tyr Lys Pro Asn Ser Leu Val Ala Lys Met				
160		165		170
gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata				1061
Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile				
175		180		185
cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag				1108
Gln Pro Ile Leu Val His Asn Asp Gln				
190		195		
atgtacaaca aaatatcaat caccacggca cacatctatg ttaaaaataaa atgtaaaatg				1168
catagtcaac caatcgaaaa cgacgattaa ggtggaaagga gttttacaat tggggcagagg				1228
attacatgta gcagtagttg gtgcgacagg cgctgttagga cagcaaatgt taaaaacact				1288
agaagacagg aattttgaac tggataaaact gactttatta tcctaaaaac gttcagcagg				1348
tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgac ctgagagctt				1408
tgaaggcgtc aacatcgac ttttcagcgc cggggaaagc gtttcgcagg cgcttgctca				1468
cgaggctgtc aaacgcgggg cgatcgatcat tgataatacg agcgcgttcc ggatggacca				1528
aaacactccg ctcgtcgatc ctgaggtcaa tgaggaagat ttgcacaagc acaacggat				1588

<210> 95

<211> 196

<212> PRT

<213> Bacillus licheniformis

<400> 95

Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly Leu Thr Gly Ser His				
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				15

Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys				
20		25		30

Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp				
35		40		45

Thr Arg Phe Gly Glu Gly Glu Trp Val Arg Arg Ile Glu Glu Leu				
50		55		60

Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly				
				Page 133

65

70

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75

80

Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn
 85 90 95

Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met
 100 105 110

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile
 115 120 125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu
 130 135 140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro
 145 150 155 160

Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met Asp Leu Leu Val Pro
 165 170 175

Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile Gln Pro Ile Leu Val
 180 185 190

His Asn Asp Gln
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<210> 96
 <211> 2167
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (501)..(1871)

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tatgatcgcc ttttcttca caaatggacc ggtcatcaat tatgatacag cgaaacagtc	180
tgacctcgga ctgtttgccg aatattataa aggaatggcc gatgaaggcg tgtttctgcc	240
gccttcacag tttgaagggc tgttcttgtc aaccgctcat acggatgacg acattgagca	300
tacgattaaa gctgctgaac gcgtattcga aagaatcagc cgctccagat aaagaaaaagg	360
gctgccggac attgccggcg gctcttttt gcatggtgcc gaaaacggct gctgatTTT	420
ctgttcatat tctgcctgct ttccacatac atctttactg acatctaatt ttaaaaatta	480
ggtgaaggga ggatatcagt ttg ccg caa aac aat cgt ttg caa tt tct gta	533
Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val	
1 5 10	

gaa gag tca atc tgt ttt caa aaa gga cag gaa gta tcc gaa tta tta	581
Glu Glu Ser Ile Cys Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu	

10295.204.ST25.txt

15	20	25	
tcg att tca ttg gat cct gac att acc gtt cag gaa gta aat gat tat			629
Ser Ile Ser Leu Asp Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr			
30	35	40	
gta tcc ata cga ggg tca tta gag ctg acà ggc gaa tac aac ata gat			677
Val Ser Ile Arg Gly Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp			
45	50	55	
caa acc cg ^g gag tat gca gag ctg cct gc ^g aca agc cga ttt gta gaa			725
Gln Thr Arg Glu Tyr Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu			
60	65	70	75
gat gta aag ctg aaa ggg gac ggc agc gca gag ctg acg cat tgt ttc			773
Asp Val Lys Leu Lys Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe			
80	85	90	
cca gtg gat atc acc atc ccg aaa gac aaa gtc aat cat tta aac gac			821
Pro Val Asp Ile Thr Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp			
95	100	105	
gta ttt gtt ttt att gac gct ttc gat tat cag ctg aca gat gc ^g agg			869
Val Phe Val Phe Ile Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg			
110	115	120	
atg ctg acg att cag gct gat ttg gc ^g att gaa ggc ctc ttg aat gt ^g			917
Met Leu Thr Ile Gln Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val			
125	130	135	
agc ggt gaa gc ^g ggt gaa gaa gaa ccg cgc act atg cct gc ^g gcc gtc			965
Ser Gly Glu Ala Gly Glu Glu Pro Arg Thr Met Pro Ala Ala Val			
140	145	150	155
cat ccg gaa gag gag ctc gaa cct gcc tac aga tca cct tca aac gac			1013
His Pro Glu Glu Glu Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp			
160	165	170	
gaa gat cag ggt gaa gag aaa gaa tat ttg atc cag ctt gac aga cct			1061
Glu Asp Gln Gly Glu Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro			
175	180	185	
tac gaa gag cag gac gaa gaa cag gc ^g gaa gaa cat gat acc ggt gag			1109
Tyr Glu Glu Gln Asp Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu			
190	195	200	
gaa acg gtt ccg att tac cag tcg ttt ctc gga aac gac aca gag gaa			1157
Glu Thr Val Pro Ile Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu			
205	210	215	
gct aaa ccg ttt ttt aca gc ^g tct ttg tcg gc ^g gca gag cgt acg aag			1205
Ala Lys Pro Phe Phe Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys			
220	225	230	235
cgc gaa ata gaa aat caa aaa gaa gcc tct ctt gaa cag ccg gaa gaa			1253
Arg Glu Ile Glu Asn Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu			
240	245	250	
gaa tat aag ctg aaa aga gag aaa gt ^g gaa gag gaa ccg gaa gaa tat			1301
Glu Tyr Lys Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr			
255	260	265	
gag ctg aaa aga gag aaa gt ^g gaa gag gaa ccg gaa gaa tat gag ctg			1349
Glu Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu			
270	275	280	
aaa aga gaa gaa gc ^g gaa gaa gag ccg gag ctg tcg cac agc tct tat			1397
Lys Arg Glu Glu Ala Glu Glu Pro Glu Leu Ser His Ser Ser Tyr			

10295.204.ST25.txt

285	290	295	
caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct			1445
Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro			
300 305 310 315			
ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt			1493
Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val			
320 325 330			
gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg			1541
Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly			
335 340 345			
cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc			1589
His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro			
350 355 360			
gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca			1637
Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser			
365 370 375			
gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag			1685
Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys			
380 385 390 395			
cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa			1733
Gln Gly Glu Glu Glu Phe Thr Arg Met Cys Ile Val Gln Gln			
400 405 410			
aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag			1781
Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln			
415 420 425			
cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag			1829
Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu			
430 435 440			
gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc			1871
Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala			
445 450 455			
taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaatgag			1931
tacggtctta cgcctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgtatacg			1991
gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa			2051
cagatgatca tgctggagga aaaaggctac aggcagttcg ttccgtcta tcgaaaccgc			2111
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<210> 97

<211> 457

<212> PRT

<213> *Bacillus licheniformis*

<400> 97

Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val Glu Glu Ser Ile Cys			
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Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu Ser Ile Ser Leu Asp			
20	25	30	

10295.204.ST25.txt

Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly
35 40 45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr
50 55 60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys
65 70 75 80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr
85 90 95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile
100 105 110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln
115 120 125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly
130 135 140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu
145 150 155 160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu
165 170 175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp
180 185 190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile
195 200 205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe
210 215 220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn
225 230 235 240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Tyr Lys Leu Lys
245 250 255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu
260 265 270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala
275 280 285

Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu
290 295 300

10295.204.ST25.txt

Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp
 305 310 315 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu
 325 330 335

Ala Glu Ala Ile Asp Glu Glu Glu Ala Gly His Thr Ile Glu Ile
 340 345 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp
 355 360 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp
 370 375 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu
 385 390 395 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp
 405 410 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met
 420 425 430

Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr
 435 440 445

Ile Pro Asp Tyr Gln Asn Ser His Ala
 450 455

<210> 98
 <211> 1955
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1463)

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aaaaaggcgaa atttcatttc cttcaaatca aaaagacttt ggtgaagatc ccgcgtgaa	240
acaggggaga gccgagcgc gcctgcagca catttcaga cagattggct ccattccccg	300
aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac	360
caaacaggat gaaaaattt gtttgtccgc acagcttacc tgaatacaat aaaaataaa	420
gtatttctcg ggaaagcgca ggttcaaca agacctgccc cggttgcgtc aaaaagcatt	480
ggatttgca gtcatgtggg cgtctgtcac ggcataagcg cgccatgaat agatataaa	533
gagagaatgg tgaggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac	

10295.204.ST25.txt

Val	Leu	Glu	Arg	Ala	Val	Thr	Tyr	Lys	Asn	Asn					
1					5				10						
gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat											581				
Gly	Gln	Ile	Asn	Ile	Ile	Leu	Asn	Gly	Gln	Val	Leu	Ala	Asn		
15					20				25						
tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc											629				
Ser	Glu	Ala	Glu	Ala	Glu	Tyr	Gln	Ala	Ala	Leu	Gln	Lys	Asn	Glu	Ala
30					35				40						
aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc											677				
Lys	His	Ser	Ile	Leu	Lys	Glu	Ile	Glu	Arg	Glu	Met	Asn	Thr	Leu	Val
45					50				55						
gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att											725				
Gly	Met	Glu	Glu	Met	Lys	Arg	Asn	Ile	Lys	Glu	Ile	Tyr	Ala	Trp	Ile
60					65				70			75			
ttc gtt aat aaa aag cgc gaa gaa caa ggc ctt aag gcc gga aaa cag											773				
Phe	Val	Asn	Lys	Lys	Arg	Glu	Glu	Gln	Gly	Leu	Lys	Ala	Gly	Lys	Gln
80					85				90						
gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc											821				
Ala	Leu	His	Met	Met	Phe	Lys	Gly	Asn	Pro	Gly	Thr	Gly	Lys	Thr	Thr
95					100				105						
gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca											869				
Val	Ala	Arg	Leu	Ile	Gly	Arg	Leu	Phe	Tyr	Glu	Met	Asn	Val	Leu	Ser
110					115				120						
aaa ggc cat ctg atc gag gcg gag cgc gcc gat ctc gtc ggt gag tac											917				
Lys	Gly	His	Leu	Ile	Glu	Ala	Glu	Arg	Ala	Asp	Leu	Val	Gly	Glu	Tyr
125					130				135						
atc ggc cat acg gcg caa aaa acg agg gat tta atc aaa aaa gcg atg											965				
Ile	Gly	His	Thr	Ala	Gln	Lys	Thr	Arg	Asp	Leu	Ile	Lys	Lys	Ala	Met
140					145				150			155			
ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga											1013				
Gly	Gly	Ile	Leu	Phe	Ile	Asp	Glu	Ala	Tyr	Ser	Leu	Ala	Arg	Gly	Gly
160					165				170						
gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg											1061				
Glu	Lys	Asp	Phe	Gly	Lys	Glu	Ala	Ile	Asp	Thr	Leu	Val	Lys	His	Met
175					180				185						
gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg											1109				
Glu	Asp	Lys	Arg	Asn	Glu	Phe	Ile	Leu	Ile	Leu	Ala	Gly	Tyr	Ser	Arg
190					195				200						
gaa atg gat cat ttt ctt tca tta aac ccg ggc ctt cag tca agg ttt											1157				
Glu	Met	Asp	His	Phe	Leu	Ser	Leu	Asn	Pro	Gly	Leu	Gln	Ser	Arg	Phe
205					210				215						
ccg atc agc atc gat ttt ccc gat tac tca gtc agc cag ctg atg gac											1205				
Pro	Ile	Ser	Ile	Asp	Phe	Pro	Asp	Tyr	Ser	Val	Ser	Gln	Leu	Met	Asp
220					225				230			235			
att gca aaa cgg atg atg gcg gaa agg gaa tat cag ttc agc cct gag											1253				
Ile	Ala	Lys	Arg	Met	Met	Ala	Glu	Arg	Glu	Tyr	Gln	Phe	Ser	Pro	Glu
240					245				250						
gct gaa tgg aag ctg aaa gac cat ctg atg gcc gtc aaa agt acg gtc											1301				
Ala	Glu	Trp	Lys	Leu	Lys	Asp	His	Leu	Met	Ala	Val	Lys	Ser	Thr	Val
255					260				265						
agc ccc gcg aag ttc agc aat ggc cgt ttc gtc cgc aac ctg atc gaa											1349				

10295.204.ST25.txt

Ser Pro Ala Lys Phe Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu	270 275 280	
aaa tcc atc cgg tcg cag gcg atg aga ctg ctg atg gga gac tgc tac		1397
Lys Ser Ile Arg Ser Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr		
285 290 295		
tta aag aat gac ttg ata acc atc aaa agc cag gat ctc gac ttg aag		1445
Leu Lys Asn Asp Leu Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys		
300 305 310 315		
gaa gac gcg ccg cac gta taatggcgcg ttctttttt attttcgagg		1493
Glu Asp Ala Pro His Val		
320		
atttctggca accgctccct tcgttgtta tgatagtact gcttattgac taacgttaag		1553
aaaggaacat gatcacttga acgaacagga agtcatgaaa gagaaagcca tattagtcgg		1613
atgccagctt ccgcacgtgt ctgatgagcg ttttcatac tcgatggaag agctcgccgc		1673
gctgacgaaa acggccgacg gaacgggtgt ttccacggtc acgcagaagc ggaaccgtgt		1733
ggatgctgct acatatatcg gaaaaggaaa agtagatgaa ttggcggtgc tctgtgaaga		1793
gctgtcgccc gatgtttaa ttttaatga tgaattgtcg ccgagtcagc tgaaagcgct		1853
tgtcacaaacg cttgacgtga aaatcatcga ccggacgcag ttgatccttg atatttcgc		1913
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<210> 99

<211> 321

<212> PRT

<213> Bacillus licheniformis

<400> 99

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20 25 30	

Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu	
35 40 45	

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met	
50 55 60	

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys	
65 70 75 80	

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met	
85 90 95	

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile	
100 105 110	

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile	
Page 140	

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10295.204.ST25.txt
120 125

Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala
 130 135 140

Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe
 145 150 155 160

Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly
 165 170 175

Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn
 180 185 190

Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe
 195 200 205

Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp
 210 215 220

Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met
 225 230 235 240

Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu
 245 250 255

Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe
 260 265 270

Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser
 275 280 285

Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu
 290 295 300

Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys Glu Asp Ala Pro His
 305 310 315 320

val

<210> 100
 <211> 2082
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1607)

<400> 100
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10295.204.ST25.txt

gaattttcta aaacgcctcg tgccgaaaca tgctcaagaa tcggctataa ctttcagcgg	120
aggcgggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat	180
tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaatg	240
tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg	300
aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa	360
ttaggcatta acaatttagca ttgttaaagac ttactgaaca agtaggtctt ttttttatga	420
ataaaatcaa gccgtgccaa ttttagcggca ggcatacataa cttatttgg aacttttga	480
attttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe	533
1 5 10	
caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac	581
Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp	
15 20 25	
agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga	629
Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg	
30 35 40	
ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga	677
Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly	
45 50 55	
acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg	725
Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly	
60 65 70 75	
gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc	773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Ala Thr Ala Glu Ala	
80 85 90	
gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa	821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu	
95 100 105	
aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct	869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala	
110 115 120	
act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg	917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met	
125 130 135	
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag	965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu	
140 145 150 155	
gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag ccg cct gtc ggc	1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly	
160 165 170	
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg	1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu	
175 180 185	
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca	1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala	
190 195 200	
gcc cggttccaa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac	1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr	

10295.204.ST25.txt

205	-210	215	
ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala 220 225 230 235			1205
gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa Ala Ala Leu Leu Ile Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln 240 245 250			1253
aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu 255 260 265			1301
cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His 270 275 280			1349
ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu 285 290 295			1397
aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His 300 305 310 315			1445
ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro 320 325 330			1493
ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro 335 340 345			1541
ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys 350 355 360			1589
aaa gga gga ggg gaa aag tgacggttca ttttggttta atcggctgcg Lys Gly Gly Glu Lys 365			1637
gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg ccgtcagtga tttgcaggaa gaaagaatga aggaagcggaa agaatactat gcttccctcg ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg cgctgctggc aggcaagcac gtcatcgatcg aaaaaccat gaccctgtca ttacggatg ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga tgcgccaccg gccgatcatg aaaaaactga aggaaacatg tgaggaagga aagctggaa agatctactt gggcacggta tcgct			1697
			1757
			1817
			1877
			1937
			1997
			2057
			2082

<210> 101
<211> 369
<212> PRT
<213> *Bacillus licheniformis*

<400> 101

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln
1 5 10 15

10295.204.ST25.txt

Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile
20 25 30

Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
65 70 75 80

Thr Pro Phe Thr Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Ile
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
260 265 270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
275 280 285

10295.204.ST25.txt

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
355 360 365

Lys

<210> 102
<211> 1975
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1472)

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	ccaaaaggct gatttgatca ttgatcgact tcataatcggc agtacggat tatttgcgt	180
	cgaatcgatg gcaatgggaa aaccgttat ctgctggatc agtgattttt tgaaggatca	240
	ctatccccc gaaactgcctc ttataagagc aaatcccgcc aacattacag aggtgattga	300
	aaatgtgctt aaaaaccggg atatgctgcc ggaaatcgcc cagaaaaggaa gaaagtatgc	360
	agaagttcat catgatatgg tgaaaaacag caaaaaaaaaa ttggctgttt atcagtcgct	420
	actttcgaa tgaagttgaa caactttccc gtcgcgggat ttgtatgtaa aaaaaaaaaacga	480
	aacaagcagg tgaacaattt atg agc gat atg aca gag tta tcc ggc cag cat	533
	Met Ser Asp Met Thr Glu Leu Ser Gly Gln His	
1	5	10

att ttc ata act ggc gga gca ggc ttt atc gga tcc tct tta ata gga	581
Ile Phe Ile Thr Gly Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly	
15 20 25	

aag ctg ata gag cgc aac agc gtc acc gta tat gac aat ttt tca aga	629
Lys Leu Ile Glu Arg Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg	
30 35 40	

gac tcc ctc cgg tat aag cct tac cgg gac cat cct cac ttg aaa gtg	677
Asp Ser Leu Arg Tyr Lys Pro Tyr Arg Asp His Pro His Leu Lys Val	
45 50 55	

10295.204.ST25.txt

ctg cag gga gac att ttg gat ttg aac gcg ctt aaa aag gcg atc cag Leu Gln Gly Asp Ile Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln 60 65 70 75	725
ggg gcc agc cac att gtc cac gcc gcc ggc atc gct ggg att gac acg Gly Ala Ser His Ile Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr 80 85 90	773
gtc att caa aac ccg gtt aaa acg atg cag gtc aac atg atc ggt tca Val Ile Gln Asn Pro Val Lys Thr Met Gln Val Asn Met Ile Gly Ser 95 100 105	821
gcc aat ctg ctt gaa gcg gct gcc ggt tta acc gaa tgc aaa agg gtt Ala Asn Leu Leu Glu Ala Ala Gly Leu Thr Glu Cys Lys Arg Val 110 115 120	869
gtc tgt ttc agt aca agc gaa gtg ttc ggc caa atc gct ttc aga gcg Val Cys Phe Ser Thr Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala 125 130 135	917
cgc gag acc agt cat act gtt tta gga gcg gtg gga gaa gcc cgc tgg Arg Glu Thr Ser His Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp 140 145 150 155	965
aca tat gct gtc agc aaa ctc gcc gag gag cat atg gca tat gcc tat Thr Tyr Ala Val Ser Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr 160 165 170	1013
ttt aaa gaa ctt ggg ctt ccg acc gtc acc gtc cgc cct ttt aat gtt Phe Lys Glu Leu Gly Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val 175 180 185	1061
tat gga ccg gaa caa gtc ggc gaa ggc gcc atc aaa acg atg gtt cac Tyr Gly Pro Glu Gln Val Gly Glu Gly Ala Ile Lys Thr Met Val His 190 195 200	1109
aga gct ctg tta gat gag ccg atc tat att cac ggc gat gga acg caa Arg Ala Leu Leu Asp Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln 205 210 215	1157
atc cgg gcc tgg tgt tac gta gat gac atg atc gac gga att ttg cgt Ile Arg Ala Trp Cys Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg 220 225 230 235	1205
tgt ttg acg atg aag gaa gcc atc gga gag tct ttc aac atc ggc aat Cys Leu Thr Met Lys Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn 240 245 250	1253
gaa cgc act gtg atc acc gta tac gga ttg gca acg acg att atc aga Glu Arg Thr Val Ile Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg 255 260 265	1301
gtt ctc gga tca aaa tca caa atc ttc ttt ggg gag aaa aaa gaa gcc Val Leu Gly Ser Lys Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala 270 275 280	1349
gat att gaa ctg cgc atc cct cag gtc aat aaa gca aaa gag atg ctc Asp Ile Glu Leu Arg Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu 285 290 295	1397
ggt ttc agc gct aaa gtt gat ctg gaa gaa ggc atc aga aga acg gct Gly Phe Ser Ala Lys Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala 300 305 310 315	1445
gaa agc att aaa aaa aat ttg gat caa taagaaaaggaa ggccgtatttg Glu Ser Ile Lys Lys Asn Leu Asp Gln 320	1492

10295.204.ST25.txt

ttgaaacaat ggaaaagcga aggaaaaggta	gaattcactc tttccagct tgggggttgt	1552
ggcgaaaatg tcgttatcga agacgggtc cgcattttc atccggaaaa catctatac		1612
ggagataacg tttatatcgg ccatgacacag attttaaaag gctattataa gcatgacctg		1672
atcatcggtt caaacagctg gatcggcag caatgttta tacacggtgc cggcggggtt		1732
acaatcgag aatttgcagg aattggtccg aacgtccgga tacatgccgc ttaccatacc		1792
gatcctgata aacccgacag taccatttg tttcgccgc ttacattcgc tcctattcat		1852
attgaagaaa actgcaacat cggatcggt gcgtctatcc tagcaggcgt tacgataggc		1912
gcccactcca aaatcgagc aaatgccgtc gtcaatcgca atattcccc gtacagcata		1972
gca		1975

<210> 103

<211> 324

<212> PRT

<213> *Bacillus licheniformis*

<400> 103

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Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly Lys Leu Ile Glu Arg		
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Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg Asp Ser Leu Arg Tyr		
35	40	45

Lys Pro Tyr Arg Asp His Pro His Leu Lys Val Leu Gln Gly Asp Ile		
50	55	60

Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln Gly Ala Ser His Ile			
65	70	75	80

Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr Val Ile Gln Asn Pro		
85	90	95

Val Lys Thr Met Gln Val Asn Met Ile Gly Ser Ala Asn Leu Leu Glu		
100	105	110

Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val Val Cys Phe Ser Thr		
115	120	125

Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala Arg Glu Thr Ser His		
130	135	140

Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp Thr Tyr Ala Val Ser			
145	150	155	160

Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr Phe Lys Glu Leu Gly	
Page 147	

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165

170

175

Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val Tyr Gly Pro Glu Gln
 180 185 190

Val Gly Glu Gly Ala Ile Lys Thr Met Val His Arg Ala Leu Leu Asp
 195 200 205

Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln Ile Arg Ala Trp Cys
 210 215 220

Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg Cys Leu Thr Met Lys
 225 230 235 240

Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn Glu Arg Thr Val Ile
 245 250 255

Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg Val Leu Gly Ser Lys
 260 265 270

Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala Asp Ile Glu Leu Arg
 275 280 285

Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu Gly Phe Ser Ala Lys
 290 295 300

Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala Glu Ser Ile Lys Lys
 305 310 315 320

Asn Leu Asp Gln

<210> 104
<211> 1213
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(710)

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tgcgcccttt aatcgccatg gataagacgg aaatcatcga aaaagcgaag gaaatcgata	240
cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg cttctgcgc	300
cggaaacgcg tccgaaaaaaaa gagaaaaatcg aacactttga aagctacaca gatttcgaac	360
cgttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcggaaa	420
cggaaagatca atttgcggat ttttctaaa ggaatattca atcaaacatc tttgtctgtt	

10295.204.ST25.txt

tttgcataca attaccaaac attctttgta tgaagtcatg tggttttaca caatctatac	480
tcacaaggag gtgagaacac atg gct caa aac aac aga caa agc agt tct aac	533
Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn	
1 5 10	
caa cta ttg gtt cct ggt gct gct caa gct atc gac caa atg aaa ttc	581
Gln Leu Leu Val Pro Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe	
15 20 25	
gaa atc gct tct gaa ttt ggc gtt aac ctt gga gca gaa act act tct	629
Glu Ile Ala Ser Glu Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser	
30 35 40	
cgt gca aac ggt tca gtt gga gga gaa atc act aag cgt tta gtt tct	677
Arg Ala Asn Gly Ser Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser	
45 50 55	
ttc gct caa cag caa atg ggt gga aca caa caa taattaaaat taaaaagcaa	730
Phe Ala Gln Gln Met Gly Gly Thr Gln Gln	
60 65 70	
tggataatgg gtggggttta atccccactc ttttttatgt tctgaaaaat aggcatttcg	790
gaatacaatt gtatgaaagg attatgtata ataaaaagat ggcacaagac aaggagatgg	850
aagggttag aagagaagat ttgattgcgc cggagaagta taatgcggtt gatgaaattg	910
aaaaatttaa atttccgc gataagaccg cattgatctg ggaagatgaa tcagggcgtc	970
aagtgtcatg gtcctatgaa aaattgattg aaaaggctta caaaatcgcc agcatattga	1030
cccgttctgg actgaaaaaaaaa ggtgacaagc ttatcgat gatgccgcgg ataccggaaa	1090
cgtatgcgt gtacatggcc attttaaaag ctggaatggt ggtcatccca tgttccgaaa	1150
tgcttcgggc gaaagacttg gattacagga tcaagcatgc aggcgtcaaa ggagccgtcg	1210
tat	1213

<210> 105

<211> 70

<212> PRT

<213> *Bacillus licheniformis*

<400> 105

Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn Gln Leu Leu Val Pro	
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Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe Glu Ile Ala Ser Glu	
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Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser Arg Ala Asn Gly Ser	
35 40 45	

Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser Phe Ala Gln Gln Gln	
50 55 60	

Met Gly Gly Thr Gln Gln	
65 70	

10295.204.ST25.txt

<210> 106
<211> 1196
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(695)

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gattttaat acgattacag accgctccga tgatgttagtgc gtcggctgc gcttttatga	120
agggtatgcg cgggtccttg atcatgtgtca ccagatcaa gactatacgc tcaataaattc	180
ggcgcttgcgaaaatcgta ttgagcagac tggacagctc cgcgattttt ataaagatct	240
ggccgatccc gaatggaaca aagcgagaga catcaccgca gtcactgtgc tgtccgtcat	300
cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtttct taaaatatga	360
aatgaaataa tcgcccaccg gcgcgcctgg cttgccaatt gccaggcggtt ttttgcctt	420
tcaacaatttgc ccagcataaa aagcctcagt ccaaataaaa ctaaacaaggc agtaccaatt	480
gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg	533
Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly	
1 5 10	
gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc	581
Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe	
15 20 25	
ggc gtc cag ctc ggc tcg gac tcg gtc gct cgc tca aac gga tct gta	629
Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val	
30 35 40	
ggc ggg gaa atg aca aaa cga ctt gta cag cag gca caa gct caa ttg	677
Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu	
45 50 55	
aat ggg cat aat gac aaa taaataccct atggattatt cggccggcccc	725
Asn Gly His Asn Asp Lys	
60 65	
gctcggcgga tattcttgtt tattcgtttgcagaaggc ttttctcct tttggtaagg	785
aagtgattta gagctctctt gatttgaacc ggaaccgctt tttggcggtc cttcctccgt	845
ctgctgaccg tctttgtcat tatggttatg ttcctgaggg tttttggat taggggaatt	905
tgactccctt tcttttcca tttcttgatc aggttgagac tgatcttcat ctgaaggttt	965
ttcggcggtcc ggatgatctt ccgtatctgc ttctttatca tccgtatgct gttccggctg	1025
atcttcttctt ttcacagctt tctcctttc tcctgtgttt tcttcctgat tttgatcatc	1085
ttttttattt tcattgtcat catctttgtt tttgtcttct aattcatctt tgtggaaacg	1145
gatataacgg cctgttgaga tgccttctt ttgggctttt gcacgcgtat c	1196

<210> 107
<211> 65
<212> PRT
<213> *Bacillus licheniformis*

10295.204.ST25.txt

<400> 107

Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly Ala Glu Gln Val Leu
 1 5 10 15

Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly
 20 25 30

Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr
 35 40 45

Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp
 50 55 60

Lys
 65

<210> 108

<211> 2279

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1463)

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 ccggcttgca ccgaatgaca gcgattattt tttaatcaaa ccaaagcaact cagccttta 180
 cggcactgct cttgaaacat tgctgcatga acttcatgtc gatcattga tcatactgg 240
 gatcgcaggc aatatctgct tattatttac ggcaaacgt gcttatatgc gggagtagca 300
 gattacgatt ccgcgcgatt gcatgcctc aaacaatgaa aaagacaaca aatacgccctt 360
 gacgatgatg gaaaatgttc tgttcgccaa tatcacgacg gctaaggcga ttacctccga 420
 aacttagagc atgaaacact tcctttcatc atatagtggt agcaatgaga aaggaggcgt 480
 ttcccatca gatttatgtc gtg aaa aga ggc gat acc ctt tac caa atc gcg 533
 Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala 10
 1 5 10

aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att 581
 Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile
 15 20 25

ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc 629
 Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile
 30 35 40

gcc ggc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc 677
 Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile
 45 50 55

gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc 725
 Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg

10295.204.ST25.txt

60	65	70	75	
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cct cg ^g cca aga cg ^g aac att gaa aca aac gcc tat atc gaa cct cg ^g Pro Arg Pro Arg Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg 95 100 105				821
gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser 110 115 120				869
cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cg ^g gac Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp 125 130 135				917
ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp 140 145 150 155				965
aga cat cg ^g act acg atg atg att gtc acc aat ctc gaa aat gaa Arg His Arg Thr Thr Met Met Ile Val Thr Asn Leu Glu Asn Glu 160 165 170				1013
gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val 175 180 185				1061
aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly 190 195 200				1109
ttt aaa gac atc cat ttt gac ttc gaa tac tta agg ccc gaa gat aga Phe Lys Asp Ile His Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg 205 210 215				1157
gaa gcc tat aat cag ttt tta cgg gat gcc cgg gcc cgc ttc agg cag Glu Ala Tyr Asn Gln Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln 220 225 230 235				1205
gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp 240 245 250				1253
cag ccc gga caa tgg tat gaa gcc cat gat tac cgg gcc cac ggc gaa Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu 255 260 265				1301
att gtc gat ttc gtc gt ^g ctg atg aca tat gag tgg ggc tac agc gga Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly 270 275 280				1349
ggg ccc ccg atg gcg gta tcg ccg atc ggg ccc gtc cgg gac gt ^g atc Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile 285 290 295				1397
gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln 300 305 310 315				1445
aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggaccc Lys Leu Tyr Gly Tyr Asp 320				1493
gttggccaag accaatccgg ccccaacggg gggattgaga tcgcgagcga gaacaatgcg				1553

10295.204.ST25.txt

gcgatacagt acgatgaaac agctcaggct ccaaacttcc gctatacgga caatgccggc	1613
aaacagcatg aagtatggtt tgaagacgcc cgctcgattc aggcaaagtt tgatctgatt	1673
agggaattga atttaagggg aatcagctat tggagctcg gcctgtcctt cccgcaaaac	1733
tggctcttga tagccgatca atttaatgtt gttaaagaga cgttcccaag ttaaaggaac	1793
gttttttttc atggcagcgg atgatgatgt gatacaatat gtatggttca caaatgaatt	1853
tcttttagtag gaggacacct atgaatacag cccctttcat tgctgtcgaa ggccccatcg	1913
gcgcgggaaa aacaaccttg gccagcatgc tctccgaaaaa gctctcaactc tctttggtca	1973
aagaaatcgt cgaagaaaaac cttttcttg ataaatttttgaatgaaaaa gatgaatgga	2033
gcttcagct tgagatgtt ttcctctgca atcgctataa gcagcttcaa gataccgaga	2093
aaaagtattt gcatcatcac atgcccgttg tttcggacta tcataatttat aaaaacctca	2153
tttttgcga acggacgctg gaaggcaaaa aacttgagaa atacagaaaa atttatcagc	2213
tgcttacaga agatctgccc aaacccaaacg tcataatttata cataagagcg agtcttccaa	2273
ctttat	2279

<210> 109

<211> 321

<212> PRT

<213> Bacillus licheniformis

<400> 109

Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala Asn Arg Tyr Arg Thr			
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Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile Pro Asn Pro Asn Arg		
20	25	30

Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile Ala Gly Glu Phe Tyr		
35	40	45

Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn		
50	55	60

Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala			
65	70	75	80

Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg		
85	90	95

Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser		
100	105	110

Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr		
115	120	125

Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu		
130	135	140

10295.204.ST25.txt

Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr
 145 150 155 160

Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu
 165 170 175

Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu
 180 185 190

Asp Asn Ile Val Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His
 195 200 205

Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln
 210 215 220

Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile
 225 230 235 240

Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp
 245 250 255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val
 260 265 270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala
 275 280 285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr
 290 295 300

Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr
 305 310 315 320

Asp

<210> 110
 <211> 2011
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (252)..(1508)

<400> 110
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 ctttcccaag cccctatcac ctcccttatt tgaaggatac actttctaga ctgttcagtc 120
 aagaattatac cgcttcacgg ttcttattcac cattccagct gtaaaaaacg gcgcatgatc 180
 cttctgcaac ggtcatagac atagcataaa acccccgtgtc acatacagag gaacaaaagg 240

10295.204.ST25.txt

aagtgtgcca g ttg ttt att tat aca gtc cag ccg gga gat tca cta ttt	290
Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe	
1 5 10	
gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg	338
Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala	
15 20 25	
aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata	386
Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile	
30 35 40 45	
ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att	434
Pro Leu Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile	
50 55 60	
gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg	482
Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro	
65 70 75	
tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg	530
Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro	
80 85 90	
gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga	578
Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg	
95 100 105	
aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc	626
Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala	
110 115 120 125	
acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta	674
Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu	
130 135 140	
agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc	722
Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg	
145 150 155	
gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt	770
Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser	
160 165 170	
ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc	818
Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg	
175 180 185	
ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc	866
Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly	
190 195 200 205	
gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt	914
Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe	
210 215 220	
tca ggt ttt ctc cgc ctg ttg aaa gag cgg ctg aag ccg tcc ggc tat	962
Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr	
225 230 235	
gtg ttg acg att gcc gtt ccg ccg aaa aca aat gaa aat atc gcc tgg	1010
Val Leu Thr Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp	
240 245 250	
ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc	1058
Leu Lys Gly Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile	
255 260 265	

10295.204.ST25.txt

ttc atc atg gca tac gac tgg cac cac ggg aca agc gag ccc ggc ccc Phe Ile Met Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro 270 275 280 285	1106
att gct ccg atc aat gaa gtc cg ^g caa aca att caa ttt gct ctc cgc Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg 290 295 300	1154
cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt cc ^g ctt tac ggc tat His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr 305 310 315	1202
aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala 320 325 330	1250
aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca cc ^g att caa Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln 335 340 345	1298
tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln 350 355 360 365	1346
ggc aga cgg cat gtc gta tgg ttt gaa gac gca cc ^g agc atc gga aaa Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys 370 375 380	1394
aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc gtc tgg Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Val Trp 385 390 395	1442
cag ctc aca ctc agt ttt cc ^g caa gga aca tgg ctc ttg acc aaa ttc Gln Leu Thr Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe 400 405 410	1490
ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata Phe Arg Val Arg Lys Val 415	1538
acaaccgaa taatcccgct aacgaatttt gatactaaag atgtgtcctt cacacaataa caaattt ^g aa aggaatgttt gcgattgaat aatgcgatcc atgaaacatt ggagctgcatt gagctgttaa tgttaaaaaa cctttgtctg acaaagtcat caacaatgac gggaatggtt caggatcaag agttcgcga catcttgag cgtgatgcat cccaaacaaa gcatcagatc gagcatttac aaggcttatt gtcagtgaga ggtgaaaccc tatgaaccaa ttcatccaa acatgacagg catgggcgcg atgactgaac aagtcttgc caccgatttt ttaatctcgg caaaaaccgg tgtcaaaaac attgccacag ctatcacgga aacatcttct ccagaagtgc gcgaaacgct taagcagtat tt ^a acgacg cgattgacac ccatgaacag atc	1598 1658 1718 1778 1838 1898 1958 2011

<210> 111
<211> 419
<212> PRT
<213> *Bacillus licheniformis*
<400> 111

Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe Val Ile Gly
1 5 10 15

10295.204.ST25.txt

Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala Asn Gly Leu
20 25 30

Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr
35 40 45

Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg
50 55 60

Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr
65 70 75 80

Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro
85 90 95

Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg
100 105 110

Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu
115 120 125

Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu
130 135 140

Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro
145 150 155 160

Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu
165 170 175

Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp
180 185 190

Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile
195 200 205

Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe
210 215 220

Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr
225 230 235 240

Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly
245 250 255

Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met
260 265 270

Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro
275 280 285

10295.204.ST25.txt

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro
 290 295 300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr
 305 310 315 320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp
 325 330 335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr
 340 345 350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg
 355 360 365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln
 370 375 380

Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Val Trp Gln Leu Thr
 385 390 395 400

Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe Phe Arg Val
 405 410 415

Arg Lys Val

<210> 112
 <211> 2014
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (558)..(1511)

<400> 112	60
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gccggggtca actgccgttt taaagccat atggtctcct gccggacaag cgggtgtca	180
catggccgaa aaaatatagc attccccttc cgcccgctcc atggctgtgt acataccggc	240
aagcggccct ttccctctgt acgggtcgat atcttccagc accgcttttt tccc gagttc	300
tataaaccgc tccgtcaagc ccggacggct caatatcagg acgtcgcttc ccagcgcctg	360
tttgaccat tgataaagcg gcttgccctt ccagcggca aacgccttcg gttccccaaa	420
acggcgcgaa agccccctg ataatatgac atgtatttct ttccatacggc tcaaccttcc	480
ttcgcgtgtt cctgcctgcg aacatcatag caaaacttta gaaatccgaa caagtctgta	540
aatctcttt ttcaaaaggc atggcgggtt tcatttatgc atattgttagt tgtaacattt	590
atagggggct ggtcacc atg aaa aca tcg ggt tcg ctg cct tat ttt	
Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe	

10295.204.ST25.txt

1

5

10

caa gat tta tca cag gaa aac ctt ttt tta aaa gct gag ctg gca aga Gln Asp Leu Ser Gln Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg 15 20 25	638
tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa Ser His Gln Leu Ile His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys 30 35 40	686
aat cat aag ctc agc cg ^g gaa aac gca gca atg aaa cag cag ctt cag Asn His Lys Leu Ser Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln 45 50 55	734
cag ctg tca ttc gaa ctg gag cg ^g att tcg gca aac aag gaa gac aag Gln Leu Ser Phe Glu Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys 60 65 70 75	782
tcg gcc gaa acg ctc aac cg ^g ata aaa agc gaa ttg ctg agt aaa atc Ser Ala Glu Thr Leu Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile 80 85 90	830
gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa Val Val Leu Gln Glu Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln 95 100 105	878
gag ata gaa gaa aag cac cg ^c ctt cat tta aca aat gta aaa gcc gaa Glu Ile Glu Glu Lys His Arg Leu His Leu Thr Asn Val Lys Ala Glu 110 115 120	926
gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat Glu Glu Lys Lys Ser Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His 125 130 135	974
gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa Ala Glu Arg Glu Lys Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys 140 145 150 155	1022
aac gct gca tac gaa aat gcc cg ^c ctg aaa gat gaa ctt cat gct aaa Asn Ala Ala Tyr Glu Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys 160 165 170	1070
agt ctt cag ctc aaa caa atc gaa act gat gtt gc ^g gta tta aaa gag Ser Leu Gln Leu Lys Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu 175 180 185	1118
cg ^g gtg acg gaa acg aaa agc cg ^g ctt ttg gag gct gaa aaa aca aaa Arg Val Thr Glu Thr Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys 190 195 200	1166
gaa g ^c ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat Glu Ala Leu Phe Tyr Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp 205 210 215	1214
gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt Glu Ser Asp Lys Trp Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe 220 225 230 235	1262
cag cag acg gag aag gc ^c ctt gaa caa aac gag gag gtt ttt gaa cg ^g Gln Gln Thr Glu Lys Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg 240 245 250	1310
aca gaa cag atc gag gc ^c gtg ctt caa act gtt aca gag caa gtt gat Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp 255 260 265	1358
cag ctc caa caa caa ttg agc gc ^c att caa caa aat tat acg aaa atg Gln Leu Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met	1406

270

275 10295.204.ST25.txt
280

gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro 285 290 295	1454
ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys 300 305 310 315	1502
cct tta aat taaaataccac ttttaggaat aatttggttt ttacaaaaaa Pro Leu Asn	1551
accgcttgag tagattgtct caagcagttg attggcgcc ggcgtataaa gcggccgcct ttatgttccc ttaaaatgga aacgctatct gaaaaagcaa gggtttgacc tattgctgct ctgtctcagt agaaatctca ccctctaata tatattgacc gcggtatggt ttttgactt ccgggtacat ttaaatcagg cttgcataa aggttgtcat attagggatc tcaagtccgc tctcttttc gattttttt tgaagttcg agctttgat ggccgcatta tggcgttta atgttttaat cgccgcttca cgcaatttt cagctttga gcctggacgt gctgtacccc ttctgcgcct tgcgttcca tctggaattc cggcaggcag tgaggaggtt tgccggagaag tctgctgctg gttctttga gatgcttgcg gctgctgttgc 2014	1611 1671 1731 1791 1851 1911 1971

<210> 113

<211> 318

<212> PRT

<213> *Bacillus licheniformis*

<400> 113

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Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg Ser His Gln Leu Ile 20 25 30

His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser 35 40 45

Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu 50 55 60

Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu 65 70 75 80
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Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu 85 90 95

Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys 100 105 110
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His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Ser 115 120 125
--

10295.204.ST25.txt

Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys
 130 135 140

Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu
 145 150 155 160

Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys
 165 170 175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr
 180 185 190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr
 195 200 205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp
 210 215 220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys
 225 230 235 240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu
 245 250 255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln
 260 265 270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr
 275 280 285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val
 290 295 300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn
 305 310 315

<210> 114
 <211> 2341
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1838)

<400> 114
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 agcccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg 180
 aagaagcggt agatcaaaat aaaaaagaaa cagaagcttt attttctat aatcccgaca 240

10295.204.ST25.txt

tcgcttctga tgactggatt aaaacgagaa aagtcgtgaa gcgcattcggc aatcatgtct	300
ttgcgtatca gaaaggcgttc agggccattc gccttgctg ctttttttgt gcgattctt	360
cttacgcatt atcatcttc acagcccaag aaaaaattta ttttgatac tttatgaaaa	420
tcaattttca attaaaaaga aaataatttt tagacttgtc tcataatgatg ggataaaccc	480
gtgagacaag gagagaccc tc atg aac cgt ttt gta aaa gga atc gtt ctt ctt Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu	533
1 5 10	
tcg cta gct gct ttt gca gaa tgt ctt gaa ttc gtc atc aac atg Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met	581
15 20 25	
att ctt gca cggtt ggc gag cat ggc atg ggg ctc tac atg agt Ile Leu Ala Arg Glu Leu Gly Glu His Met Gly Leu Tyr Met Ser	629
30 35 40	
gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg Val Leu Pro Ser Ile Phe Leu Val Val Ile Ala Ser Leu Glu Leu	677
45 50 55	
ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His	725
60 65 70 75	
gaa agc atg ctg aaa cat gca ttg cggtt atg act gcg gtc tgc acg gtt Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val	773
80 85 90	
ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe	821
95 100 105	
gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro	869
110 115 120	
acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln	917
125 130 135	
caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln	965
140 145 150 155	
ctc atc ggc ttg ttt tta ttt caa tgg tat tcc ttt gaa ttg gat Leu Ile Gly Leu Phe Leu Phe Gln Trp Tyr Ser Phe Glu Leu Asp	1013
160 165 170	
act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc Thr Ser Leu Leu Ile Ser Leu Phe Val Leu Val Ala Ser Glu Val Val	1061
175 180 185	
gtg ttt gtt tat ttg ttt tcg cag ttt gtt ttg gtc agg cgt gcc gct Val Phe Val Tyr Leu Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala	1109
190 195 200	
caa aaa ggg cag cag atc cac ttg cgg aga aac gat gtt tta aaa cgc Gln Lys Gly Gln Gln Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg	1157
205 210 215	
ctg ctc act gtt tcg atc ccg acg acg ggg ctg cgc gtg ttt cat gct Leu Leu Thr Val Ser Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala	1205
220 225 230 235	

10295.204.ST25.txt

gtg aca aat gcc gtc gaa cct ttt ttg gtg aag ggg acg ctg ctt gcc Val Thr Asn Ala Val Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala 240 245 250	1253
gct ggc gta tca aga aca tcg gcc atc gac cag ttc ggc atg ctt tcg Ala Gly Val Ser Arg Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser 255 260 265	1301
gga gtt gcg atg aca atc ggc ttt ttt ccg gct ttt atc gcc cat tca Gly Val Ala Met Thr Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser 270 275 280	1349
ctg atg gtc gtc atg atc ccg agc att tct gaa agc tac gct tac gag Leu Met Val Val Met Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly 285 290 295	1397
caa tac gaa aga gtc atc aaa cgg att aaa cag gcg atc ttt att acg Gln Tyr Glu Arg Val Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr 300 305 310 .315	1445
ctg ttt tac ggc ata ccg tcc gtc atg gtg atg tat cac ttt gca gag Leu Phe Tyr Gly Ile Pro Ser Val Met Val Met Tyr His Phe Ala Glu 320 325 330	1493
ccg ctg acc cat tta ttt ttc gat tcg gtc aag gcg tcg ttt tac ctt Pro Leu Thr His Leu Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu 335 340 345	1541
aaa atg ttg tgg ccg tat ttt tta ttc cac ttt ttt gcg atg cct ttt Lys Met Leu Trp Pro Tyr Phe Leu Phe His Phe Ala Met Pro Phe 350 355 360	1589
cag gcc tgt tta atc gga atg ggg ttg gcc aaa gat gct ttt tat cat Gln Ala Cys Leu Ile Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His 365 370 375	1637
aac gtt tgg gcc agt gtc tta tcg ttt ttg atg atg tat gtt ctc ggg Asn Val Trp Ala Ser Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly 380 385 390 395	1685
tcc atg cag act ttg cag atg acg ggg atc att ctt gcg atg aat acc Ser Met Gln Thr Leu Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr 400 405 410	1733
ggg atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu 415 420 425	1781
ctg ggc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile 430 435 440	1829
gaa agc cgc tgatggatcc tcttcatagt tttagcttt gcggggaaagc Glu Ser Arg 445	1878
taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc	1938
ctgctgttt ttaccgggtt attcgatattt cagccgcagg catctgaaaa acaagcttcg	1998
ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc	2058
cagaagacga tcgttcattt ttggacgacc tggtgccccgc catgccgtga agagcttccg	2118
cgattccaat cctactatga aagcaagcaa tccggcgtca agctcgtgac cgtaattta	2178
ctgaatgccg aaaagaacga acagaaggtaa acacagttt ttaaagcaaa caagctgaca	2238

10295.204.ST25.txt

tttccgatcg ttttgacaa aaagggtgag atgatgaaag catataaagt catgacaatt 2298
cctacgactt ttttctttaa tgaaaaagga gagctggaga aaa 2341

<210> 115
<211> 446
<212> PRT
<213> *Bacillus licheniformis*

<400> 115

Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu Ser Leu Ala Ala Phe
1 5 10 15

Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met Ile Leu Ala Arg Glu
20 25 30

Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile
35 40 45

Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser
50 55 60

Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys
65 70 75 80

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala
85 90 95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro
100 105 110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr
115 120 125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile
130 135 140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe
145 150 155 160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile
165 170 175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu
180 185 190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln
195 200 205

Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser
210 215 220

10295.204.ST25.txt

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val
225 230 235 240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg
245 250 255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr
260 265 270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met
275 280 285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val
290 295 300

Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile
305 310 315 320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu
325 330 335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro
340 345 350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile
355 360 365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser
370 375 380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu
385 390 395 400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu
405 410 415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu
420 425 430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg
435 440 445

<210> 116

<211> 1417

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (420)..(914)

<400> 116

10295.204.ST25.txt

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tgaggtgaca	atcggaatgc	ccgcctggtt	gatgcgcctca	atatcccgtat	aatcggtct	120
gacagagact	tcgaacatgc	cggcaagctc	cttgcctgc	acttggcggtt	tattaatcaa	180
taaaaatcaca	atggccaaaa	gccggtaat	tttcaactgca	gatccctcac	attcatcttg	240
tgcagcctct	tttttctgc	tatttcatt	ccatagcgca	caccattctg	ggatatcatg	300
acaaaaaaaga	ggatctcatc	acccatttat	ctagaaaacc	actttcagg	ttacgatttg	360
tacagtttgg	acataactc	ctaaaaaaag	gaggtttaa	aaacatcata	ttttat	419
ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cg	Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg	5	10	15		467
1						
tcg gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cg	atc Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile	20	25	30		515
atc ctt ttt tcg gga att ttc gtt ttt ctg ctg acg atg agc gca ctt	Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu	35	40	45		563
50						
cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc	His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu	55	60			611
atc ttg acc gtc tat gcg ctg aag cat gtg tcg atc gaa aat cgg ggc	Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly	65	70	75		659
80						
gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc	Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu	85	90	95		707
100						
ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag	Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln	105		110		755
115						
ctg cag act gcg gtt tca gac ggg ggt tcg gca gct tac ggc gcc ctt	Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu	120		125		803
130						
ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt	Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val	135		140		851
145						
tat tat gtc ggt ttc tct ttt gtt tta aaa aaa ggc aga acc gaa	Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu	150		155		899
160						
gaa aag cgc tca gct taaaaaggca aactcggaa attgagtttgcctttaaac	Glu Lys Arg Ser Ala	165				954
170						
tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctggctt						1014
ccggagaata aaaaatggaa gtccctgccc ttcttgattt gacgagacga aggttttta						1074
aaaacctgag ctggtgagaa acggttgact gcaggagact cagttctct gctatttcat						1134
taaccgaatg ctcgccttgt gagagcaggt gaagaatttt gattctcggtt gggtcagaga						1194
gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccccacct						1254

10295.204.ST25.txt

gtttttctgt tgtttcttga ttgtgctcac tcacatgtttt cacctttcc gcgcgacttt 1314
 tacctccata tcatacatacca aaacataccg gttgaaaagt tttaacggat caagtcgaaa 1374
 acagcgttcc ttgaagcgct tctacatatac ttgcagcaga cct 1417

<210> 117

<211> 165

<212> PRT

<213> *Bacillus licheniformis*

<400> 117

Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
 1 5 10 15

ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
 20 25 30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
 35 40 45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
 50 55 60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
 65 70 75 80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
 85 90 95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
 100 105 110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
 115 120 125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
 130 135 140

Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
 145 150 155 160

Glu Lys Arg Ser Ala
 165

<210> 118

<211> 2353

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1850)

10295.204.ST25.txt

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ggcgattc tcgaacaacg acattaatct gttggcccaa gcggtttacg gtgaagcgcg		180
cggagaacgg tatgacggcc aggttgcgt tgtagctgtt atattaaaca ggctcgatag		240
ccctacgttc ccgaatacgg tggcggcgt tatcttgaa ccgcttgcac ttacagctgt		300
cgcggacgga cagattata tgacgcccga tgaaacggcg aaaaaagccg ttcttgacgc		360
catcaacggc tggatccat cagaaaatgc cacttactat tttaccctg acacggccac		420
tagctcatgg atttggggca gacctcaaataaataaaggatc ggttaacaca ttttctgtga		480
ataaaagcga ggtgctataa atg atc aga gga att tta atc gcc ctt tta ggt		533
Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly		
1 5 10		
gtc gcc atc gtc gga aca agc tat tgg ggc tat aaa gaa cat cag gag		581
Val Ala Ile Val Gly Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu		
15 20 25		
aaa gac gcc gtt ttg ctt cat gcc gaa aac aac tat caa agg gca ttt		629
Lys Asp Ala Val Leu Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe		
30 35 40		
cac gac tta act tat cag gtg gat cag ctg cat gat aaa atc ggg agc		677
His Asp Leu Thr Tyr Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser		
45 50 55		
acg ctt gcg atg aac agc aaa aaa acg ctg tct ccc gct ttg gcg gaa		725
Thr Leu Ala Met Asn Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu		
60 65 70 75		
gtc tgg aaa acg act tct gaa gcg cat aac aat gtc agc cag ctg ccg		773
Val Trp Lys Thr Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro		
80 85 90		
ctg acc tta atg ccg ttt aac aag acc gaa gag ttt ttg gca aag gtc		821
Leu Thr Leu Met Pro Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val		
95 100 105		
gga gat ttc agc tac aaa gca gcc gtg cgc gat ctt gac aaa gag ccg		869
Gly Asp Phe Ser Tyr Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro		
110 115 120		
ctc aat aaa aaa gag tac gct tct tta aat cag cta tat gaa aat tca		917
Leu Asn Lys Lys Glu Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser		
125 130 135		
aag gat ata caa aat gaa ctg cgt aat gtc cag cat ttg att att gac		965
Lys Asp Ile Gln Asn Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp		
140 145 150 155		
aaa aat ttg aga tgg atg gat gta gaa ctt gcg ctc gcg tcc ggc caa		1013
Lys Asn Leu Arg Trp Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln		
160 165 170		
aaa caa agc gac aat aag att att aat ggc ttt aaa acc gtt gaa aaa		1061
Lys Gln Ser Asp Asn Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys		
175 180 185		
agc gca agt gca ttt tcg gat acg gat tta ggc gcg aca gag atg acg		1109
Ser Ala Ser Ala Phe Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr		
190 195 200		

10295.204.ST25.txt

aac acg aaa aaa gag cag caa ggg tac gac cat tta caa ggc aaa aga Asn Thr Lys Lys Glu Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg 205 210 215	1157
ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp 220 225 230 235	1205
aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg 240 245 250	1253
gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile 255 260 265	1301
tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa Tyr Met Asp Ile Thr Glu Lys Gly Tyr Pro Val Tyr Leu Ile Gln 270 275 280	1349
aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn 285 290 295	1397
aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu 300 305 310 315	1445
aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe 320 325 330	1493
gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc Val Pro Val Gln Asp Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile 335 340 345	1541
aag gtc gcg ctt gac gac ggc gag att acc ggg ttt aat gca aag gat Lys Val Ala Leu Asp Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp 350 355 360	1589
tcc tta atc tcc cat aaa aaa aga gac ttg ccg aag ccc aaa cta acg Phe Leu Ile Ser His Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr 365 370 375	1637
cct gaa aaa gcg aaa gca agc ctg aat ccc aac gta aaa gtt cag gag Pro Glu Lys Ala Lys Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu 380 385 390 395	1685
acg cgc ctt gct tta gtc acg aac gag ctt tcg caa gaa gtg ctc tgc Thr Arg Leu Ala Leu Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys 400 405 410	1733
tac gaa att ctc ggc acg att gaa aac gat aca ttc cgc atg ttc atc Tyr Glu Ile Leu Gly Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile 415 420 425	1781
aat gcc aat gac ggc acg gaa gag aag gtt cag aaa atg aaa agc gca Asn Ala Asn Asp Gly Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala 430 435 440	1829
gaa ccg ata tac aac gac ttg taaaaacgat agatcaaagg gaaaaggcga Glu Pro Ile Tyr Asn Asp Leu 445 450	1880
taacatgcct ttccctttt agcattcgga ataattcgcc ctaaacattt ccatactgaa catatggcgcg gaacgtccgc cggtaaattg aaaatgcccg gggccataaa ttttccggc	1940 2000

10295.204.ST25.txt

agcggaggaa taatatgaaa acaatcgAAC ggttattttta agatactc gtcgtacaga	2060
cggcattttt aatcagcgtg cagttttttt ttcatttctc caaggctgag ccttatctgt	2120
caaaggtcgt gcagtatgaa ggcgtgaaca acatgaaaat cggcgaatgg atcgagacat	2180
ttaagccgta attcacgcta aaatctcccc ttttcgcct aatacatgtat acaatcctat	2240
aaggagtacc agatagcaag gagaggaatt atggaaaaga aattatgcat tgcaatagac	2300
ggccctgcgg cagccggaaa aagcaccgtg gcgaaaaatcg tggccagaaa aaa	2353

<210> 119
<211> 450
<212> PRT
<213> *Bacillus licheniformis*

<400> 119

Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly Val Ala Ile Val Gly
1 5 10 15

Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu Lys Asp Ala Val Leu
20 25 30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr
35 40 45

Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn
50 55 60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr
65 70 75 80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro
85 90 95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr
100 105 110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu
115 120 125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn
130 135 140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp
145 150 155 160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn
165 170 175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe
180 185 190

10295.204.ST25.txt

Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu
195 200 205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu
210 215 220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile
225 230 235 240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile
245 250 255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr
260 265 270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys
275 280 285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe
290 295 300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser
305 310 315 320

Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp
325 330 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp
340 345 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His
355 360 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys
370 375 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu
385 390 395 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly
405 410 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly
420 425 430

Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala Glu Pro Ile Tyr Asn
435 440 445

Asp Leu
450

10295.204.ST25.txt

<210> 120
<211> 1355
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (249)..(1355)

10295.204.ST25.txt

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aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln 210 215 220	914
atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val 225 230 235	962
gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val 240 245 250	1010
acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt aaa gta agg Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg 255 260 265 270	1058
aca agt cac aag cta tcc ctc gga tca tta acc atg ccg atc tgg ggc Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly 275 280 285	1106
ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu 290 295 300	1154
aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu 305 310 315	1202
aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys 320 325 330	1250
aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln 335 340 345 350	1298
gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca Asp Lys Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala 355 360 365	1346
cac cac gag His His Glu	1355

<210> 121
 <211> 369
 <212> PRT
 <213> Bacillus licheniformis

<400> 121

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys
1 5 10 15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg
20 25 30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val Phe Leu
35 40 45

10295.204.ST25.txt

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
85 90 95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu
115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly
195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
260 265 270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser
275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His
290 295 300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
305 310 315 320

10295.204.ST25.txt

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
 325 330 335

Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln Asp Lys
 340 345 350

Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala His His
 355 360 365

Glu

<210> 122
 <211> 2120
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1625)

<400> 122	60
aactaacggtaaagaaaatct ttgtattcgg cgatcaattc ggaaggggag gaagcattgt	120
ttaccaagat ctcggcttaa aggcgacaaa gctgacaaag gaaaaagcaa tcgacgaagg	180
cccggtac acgagcattt ccttagaaaa gctgcctgat ttcgctggag attatatatt	240
tataggacct tggaaatcaa gcggagacga cagcgccgtg cttaatacat ccatttgaa	300
gaaccttggg gcggtaaaaa accaacatgt ctataaaatc gaccctgtcg gcttctat	360
ttccgatccg atttcattag agggccagct cgaattttt acagaaaact taacaaaata	420
gaagaacttc cgccgttca ggcggaaagt tttttgcgc gcgaaaccgg ggtgaaccct	480
cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata	533
tgctattgtg ggagggatca ttg atg gca ttc atc aac atc aaa ccg gag tta	
Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu	
1 5 10	
aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg	581
Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro	
15 20 25	
ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt	629
Leu Leu Ile Ser Ala Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe	
30 35 40	
ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca	677
Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr	
45 50 55	
tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa	725
Tyr Glu Gln Leu Gln Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu	
60 65 70 75	
cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag	773
Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys	
80 85 90	
gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc	821

10295.204.ST25.txt

Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile
95 100 105

atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga
Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly
110 115 120

869

gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc
Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
125 130 135

917

aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac
Asn Glu Trp Ile Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr
140 145 150 155

965

tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc
Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu
160 165 170

1013

gat att ttt tca tca aca aag ctt tcc gtc gtg ccg atc gtt aat ccc
Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro
175 180 185

1061

gac ggt gtt gac ctt gta ctt aac ggc ccc ggt cat ctt ggg atc gcg
Asp Gly Val Asp Leu Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala
190 195 200

1109

aga gaa gcg ctg gat gag atg aac gag cat cag ccg gat ttc cg gaa
Arg Glu Ala Leu Asp Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu
205 210 215

1157

tgg aaa gcc aat ata aac gga gtg gat tta aat aat cag ttt ccg tct
Trp Lys Ala Asn Ile Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser
220 225 230 235

1205

ttc tgg gag atc gaa aaa caa aga aaa ccg cct aaa tcc cct tcc tac
Phe Trp Glu Ile Glu Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr
240 245 250

1253

aga gac tac ccc gga gat gaa ccg ctg aca gaa ccg gaa gcg gca gcg
Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala
255 260 265

1301

atg agg gat tta atc gca aac gag ccg cct gac ccg ctt gtg gcg ctt
Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu
270 275 280

1349

cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct
His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro
285 290 295

1397

cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat
Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr
300 305 310 315

1445

aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg tt
Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe
320 325 330

1493

att cat tat tac gga aga gaa gga tat act gtt gaa ctt ggc aaa gga
Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly
335 340 345

1541

aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc
Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser
350 355 360

1589

aga gga ata ctt tgg gca tcc tgt ttt gaa agc tgaaactttt
1635

10295.204.ST25.txt

Arg Gly Ile Leu Trp Ala Ser Cys Phe Phe Glu Ser
 365 370 375

cacggtaaaa atcgtaaatt agacagccaa acatttatgg agggagaatg gccgggttga 1695
 gagtttcatt attgattatt gccgctctga tggccgtggc tgccgctggc tgcacgccc 1755
 agcatcaaga aggatcaaaa agcgttcatc atgaggagcc ggaagggaaa agagaaagcg 1815
 gtgcagcagt aaaagataaa aaagtgatag cgctgaagga ccggcacttt gatgagacgg 1875
 caggatggct tgataatgaa accgttatat acaccgcaac cgatccggc ggaggaagt 1935
 aaatcaaatc atatgatata tttaaaggga cgggcaaaac gatctacaag acagatgaca 1995
 ggctgatagc gtcggaagtc aacagtgaaa aaggcatgat tcttatccaa accgcccggaa 2055
 acggctctga aatgaagtta actttgctta atttacaggg gaaacagctg tttgcaaaaa 2115
 aattt 2120

<210> 123
<211> 375
<212> PRT
<213> *Bacillus licheniformis*

<400> 123

Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu Lys Gln Asn Met Glu
 1 5 10 15

Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro Leu Leu Ile Ser Ala
 20 25 30

Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe
 35 40 45

His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln
 50 55 60

Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys
 65 70 75 80

Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu
 85 90 95

Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser
 100 105 110

Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly
 115 120 125

Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr
 130 135 140

Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys
 145 150 155 160

10295.204.ST25.txt

Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser
165 170 175

Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu
180 185 190

Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp
195 200 205

Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile
210 215 220

Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu
225 230 235 240

Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly
245 250 255

Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile
260 265 270

Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu
275 280 285

Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp
290 295 300

Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr
305 310 315 320

Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly
325 330 335

Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro
340 345 350

Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser Arg Gly Ile Leu Trp
355 360 365

Ala Ser Cys Phe Phe Glu Ser
370 375

<210> 124
<211> 1597
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (342)..(1094)

<400> 124

10295.204.ST25.txt

ccttttttat ttcctaaat ttgcggaaaag ccagttaatt tatcccatat atcagaaggaa	60
aaagcgatgg tcatctcaaa actgtAACCA attatTTCT tgatagtgtg gctgcgacta	120
ttatgcgcTG attgtttacg gtgcttgcTT tttataccat tggttcattt gaccggaaATC	180
gtgtttgtat tgcaggaatt ttgttactg ttgtgaaaa aacagcagaa gaaaaacAGC	240
gaaaaactcg cgtcttaggg cggtttcca aaaaaatgtc gtaaattcga tgcattcaatt	300
tgatgaaatc gccggccat gcggtataat agatTTGTG a atg aaa gat tca atg Met Lys Asp Ser Met	356
1 5	
ttg aaa gag agt ggt tac atc atg ggc cgt aaa tgg aac aat ata aaa	404
Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys Trp Asn Asn Ile Lys	
10 15 20	
gag aag aaa gCG tcc aag gat gCG aat acg agc cga atc tac gCG aag	452
Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser Arg Ile Tyr Ala Lys	
25 30 35	
ttc ggc cgc gaa atc tat gtg gCG gca aag cag gga gag ccc gat ccc	500
Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln Gly Glu Pro Asp Pro	
40 45 50	
gaa ctg aac cag aac ctg aaa ttc gtg ctt gag cgc gcc aaa aca tac	548
Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu Arg Ala Lys Thr Tyr	
55 60 65	
aat gtc ccg aaa gCG att att gag cgg gCG atc gaa aaa gCG aag gGC	596
Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile Glu Lys Ala Lys Gly	
70 75 80 85	
ggc tct gag gaa aat tac gac gag ctg cgc tat gaa ggc ttc ggt ccg	644
Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr Glu Gly Phe Gly Pro	
90 95 100	
aac gga gCG atg gtg atc gtt gac gCG ttg aca aac aac gtc aac cgc	692
Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr Asn Asn Val Asn Arg	
105 110 115	
acg gct gcc gat gtg cgc tcc aca ttt ggc aaa aac ggc gga aac atg	740
Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys Asn Gly Asn Met	
120 125 130	
gga gtg agc gga tct gtc gct tac atg ttt gat ccg acg gcc gtc atc	788
Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp Pro Thr Ala Val Ile	
135 140 145	
ggc ttt gaa gGC aaa acg gct gat gaa acg ctc gaa tta ttg atg gaa	836
Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu Glu Leu Leu Met Glu	
150 155 160 165	
gCG gat atc gat gtc cgt gat att tta gag gaa gac gat gca gtg atc	884
Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu Asp Asp Ala Val Ile	
170 175 180	
gtc tat gcc gag ccc gat cag ttc cac gcc gta cag gag gCG ctg caa	932
Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val Gln Glu Ala Leu Gln	
185 190 195	
aac gcc ggc att act gag ttc acg gtg gcc gag ctg acg atg ctc gCG	980
Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu Leu Thr Met Leu Ala	
200 205 210	
caa aat gac gtc gcc ctt cca gag gac gCG cgc gca cag ttt gaa aag	1028
Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg Ala Gln Phe Glu Lys	

10295.204.ST25.txt

215	220	225		
ctg att gac gac	ctg gaa gat	ctg gaa gac	gtt cag caa gtt tac cat	1076
Leu Ile Asp Ala	Leu Glu Asp Leu	Glu Asp Val	Gln Gln Val Tyr His	
230	235	240	245	
aat gtc gat tta ggg gcg	taaaaagagg ccctgaaaaa	atcgggaaag		1124
Asn Val Asp Leu Gly	Ala			
250				
aaaagataga tgaacaggag	gacgacctgt ttgtctatc	ttttttatt gtaaagttaa		1184
cttgacattt tattttttg	ttaagtatac ttacgtata	gtgaacttta cattcccaat		1244
ggaggaaaga tgaaaacgtt	aataaaggaa aagcgcactt	cgctgaacat gacacaagaa		1304
gaactggcta aaaggcttaa	tgtgtcgagg caaacggtga	tttcccttga aaaggaaaaa		1364
tataaaccctt cactcgttct	ggcgcataaaa ctggctcaaa	tttttgaatg tctgattgaa		1424
gatttattta ttttgaggg	ggatgaaaat attgactgaa	acgatgacaa acatactgat		1484
cgcttagcg ggcttagaat	aggcgtgctc gggatcgcaa	ttgtttacaa agtaaacaga		1544
cgaattggaa aaaaagagag	gctgttcgat gaggcccagc	agaagattag cta		1597

<210> 125

<211> 251

<212> PRT

<213> Bacillus licheniformis

<400> 125

Met Lys Asp Ser Met Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys			
1	5	10	15
10	15		

Trp Asn Asn Ile Lys Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser			
20	25	30	
30			

Arg Ile Tyr Ala Lys Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln			
35	40	45	
45			

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu			
50	55	60	
60			

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile			
65	70	75	80
75	80		

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr			
85	90	95	
95			

Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr			
100	105	110	
110			

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys			
115	120	125	
125			

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp			
130	135	140	
140			

10295.204.ST25.txt

Pro Thr Ala Val Ile Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu
 145 150 155 160

Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu
 165 170 175

Asp Asp Ala Val Ile Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val
 180 185 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu
 195 200 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg
 210 215 220

Ala Gln Phe Glu Lys Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val
 225 230 235 240

Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala
 245 250

<210> 126

<211> 1888

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (3)..(1385)

<400> 126

ag aag gat gct gcg cgc cg^g aat gtc gat gat gct cgt aca ggc atc
 Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile
 1 5 10 15

att gct ttc tcc att cta tat ttg tcc gcc ccg ttt ttt gca gag atg
 Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met
 20 25 30

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg
 Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val
 35 40 45

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg
 Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu
 50 55 60

g^cg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca
 Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr
 65 70 75

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta
 Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu
 80 85 90 95

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc
 Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val
 100 105 110

10295.204.ST25.txt

gct gtc ggc tat gcg act ttt gcg gct ttg atc gga gcg ttc gcc gqa Ala Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly 115 120 125	383
ctg ttc act ctt tac ttt tcc tgg cag aaa aga aaa ggg gcg ctc ctg Leu Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu 130 135 140	431
gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa Ala Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln 145 150 155	479
atg ttt aaa gag ctg ttc agc tat gcc gcc cct tat gtc ttt gtc ggg Met Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly 160 165 170 175	527
ctg gcg ata ccg ctt tac cag tac att gat acg aat acg ttt aat aaa Leu Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys 180 185 190	575
gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg Ala Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala 195 200 205	623
atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc Ile Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu 210 215 220	671
gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt Ala Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe 225 230 235	719
acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg Thr Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met 240 245 250 255	767
cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt Gln Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu 260 265 270	815
ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc Leu Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu 275 280 285	863
cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu 290 295 300	911
tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac Leu Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn 305 310 315	959
aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa Lys Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys 320 325 330 335	1007
atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg Ile Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser 340 345 350	1055
att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt Ile Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe 355 360 365	1103
atc atg att aaa cgc cat gcc ggc tat tcg tat cgc aaa ctg ttt aaa Ile Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys 370 375 380	1151

10295.204.ST25.txt

cgg ttt ttg ctg atg ctg atc ctg acg gcg gtc atg ggc atc att ttg Arg Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu 385 390 395	1199
ctg ctt gtc cag gcg ctt cta agt att ttt att tca tac gaa ggc ggg Leu Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly 400 405 410 415	1247
cag atc agg tct gct gtc gtc att ttc atc aca acc gca gtg ggc ggg Gln Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly 420 425 430	1295
tca gtt tat ctg tac ttg gct tac cgt gtg aaa ctg ctc gaa aaa atc Ser Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile 435 440 445	1343
ttc ggt cag cga ttg aat cgc ttt ttc aaa aga aag gcc tcc Phe Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser 450 455 460	1385
taaaaaaggc ttttctttt atgtaaaaaaaaa aggggtgtct tcatacgatt ggataaactg ttgtcaaaca gcggctatgg ttcgagaaaaa gaagtcaaaa aaatgctgaa aaacggcg gtgcgcgtca atgatcaatt agtcaaagac gccaaaaagc acgttgaccc ggaatcagac gacatcacgg tatacggggc acccgcatg taccggaaat ttatttactt aatgatgaac aagccgcaag gagtgctgtc agcaacagaa gacagccggc aggaaacggt tgtcatttg ctcgaccgg agctgctgag gtttgagccg tttcctgtcg gaaggcttga caaggatact gagggactgc tgcttctgac gaatgacgga cagttggcac accagcttt atctccgaaa aaacacgtac ctaaaacgta tgaagtccat gtcaataagc cgattgtca agcggcactt gatcagctt aaaaagggt cga	1445 1505 1565 1625 1685 1745 1805 1865 1888

<210> 127
 <211> 461
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 127
 Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile Ile
 1 5 10 15

Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala
 20 25 30
 Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr
 35 40 45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala
 50 55 60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala
 65 70 75 80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr
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90

95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala
100 105 110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu
115 120 125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala
130 135 140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met
145 150 155 160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu
165 170 175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala
180 185 190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile
195 200 205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala
210 215 220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr
225 230 235 240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln
245 250 255

Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu Leu
260 265 270

Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu Pro
275 280 285

Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu Leu
290 295 300

Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn Lys
305 310 315 320

Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys Ile
325 330 335

Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser Ile
340 345 350

Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe Ile

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360

365

10295.204.ST25.txt

Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys Arg
 370 375 380

Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu Leu
 385 390 395 400

Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gln
 405 410 415

Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly Ser
 420 425 430

Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile Phe
 435 440 445

Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
 450 455 460

<210> 128

<211> 1852

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1349)

<400> 128

tcacttttg aatcagctgt cagacgcttt gaagctggaa aacacagctt tttaccatga 60
 ccgcgcggaa acattcgaa gatcgaaaga ccacagagaa agctatgacg ttgtgacggc 120
 acgcgctgtc gcccgcctt cggttctcag cgagctctgc cttccgcttg tgaaaaaaa 180
 cggtttattc gtagcattaa aagccgcttc ggctgatgaa gaaattgaaa cgggcaaaaa 240
 agccatcaaa acgcttggag gcaaaattga aaccgtacat tcttttcagc tgccaataga 300
 agaaagcgaa agaaacatca ttgtcatcaa aaaacaatcg cagacaccga agaaatttcc 360
 aagaaagcct ggaacaccta ataaatctcc tattgaaggt taaatttattc gttttcttca 420
 aatttcgtga tgtcacagaa ggaaaattca tgagaaaata gaattataaa aatggcagtg 480
 tttaaaggta gtgttaggtac atg aag cat tca ttc tct cgt ctc ttc gga ctt 533
 Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu
 1 5 10

ggc gac aag gaa gaa gaa gca gag att gct gaa cat gat acg aat aaa 581
 Gly Asp Lys Glu Glu Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys
 15 20 25

gaa gaa att caa gag att cca gta ggc gat ata att cct aac cgt ttt 629
 Glu Glu Ile Gln Glu Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe
 30 35 40

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca 677
 Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala

10295.204.ST25.txt

45	50	55	
acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca			725
Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr	65	70	75
60			
gag cg ^g gaa ggc caa tat gaa ctc ata gcc gga gag cg ^g cg ^c tgg cg ^g			773
Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg	80	85	90
95			
g ^c g gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat			821
Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp	95	100	105
110			
ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag			869
Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln	110	115	120
125			
agg gaa gaa tta tct tcg att gaa gag g ^c g cat gct tat gca agg ctt			917
Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu	125	130	135
140			
tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga			965
Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly	140	145	155
150			
aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg			1013
Lys Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro	160	165	170
175			
gaa gag gtg cag gaa g ^c g atc ttg aaa aaa gaa att tca gag cg ^c cac			1061
Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His	175	180	185
190			
gca aga g ^c g ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg			1109
Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu	190	195	200
210			
ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac			1157
Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp	205	210	215
220			
cgt gtc gtc aaa atg ctt gag cag gat aaa cg ^c aag cct aaa cca aag			1205
Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys	220	225	230
235			
aga aaa gcg tac agc agg gac g ^c g aga atc g ^c g atg aat acg att cg ^c			1253
Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg	240	245	250
255			
cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa			1301
Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu	255	260	265
270			
gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa			1349
Glu Glu Glu Phe Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys	270	275	280
285			
taaaagctcc ctatagagct tttatTTTT taggaaaaat atctatgggg gagcgcttat			1409
ggaatattat cgacaataatc attcattgct ttttcgatt gcttaccgta tgctcgggtc			1469
ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat			1529
cggtaaattt gaccatattc aagcatattt aacgaaatca atcacaaacc gctgcataaa			1589
tgaactgcag tctgccccca agaagcggga ggttatatc gggaaatggc ttccggacc			1649

10295.204.ST25.txt
 gcaggtggcg ctttcagctc aaatcccgac tgagtacgtt gaagagaaag aaaaggatc 1709
 ctatgcttt ctggtagtta tgagccgatt aaatcctgtt gaaagagccg ttttgatgtt 1769
 tagagaagta tttggatatc attacaagga aatttcgtcc attatcggga agtcggaagc 1829
 gaactgtcgt caaatccaca gcc 1852

<210> 129
 <211> 283
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 129

Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu Gly Asp Lys Glu Glu
 1 5 10 15

Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys Glu Glu Ile Gln Glu
 20 25 30

Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile
 35 40 45

Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His
 50 55 60

Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln
 65 70 75 80

Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu
 85 90 95

Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu
 100 105 110

Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser
 115 120 125

Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp
 130 135 140

Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr
 145 150 155 160

Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu
 165 170 175

Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile
 180 185 190

Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile
 195 200 205

10295.204.ST25.txt

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met
 210 215 220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser
 225 230 235 240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met
 245 250 255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Phe Glu
 260 265 270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
 275 280

<210> 130

<211> 1495

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(995)

<400> 130	60
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tcgtccatga gcctgatgcc gctttaacgg caaatcaata ccccgtaat ctgcaaatat	120
ccggacacac ccacgcgcgg acaaattcag attcctgtat tcggtccttt gattacgcct	180
ccgtacgtac acgtttatac gcaaggaatg tatgcaacag ccgaaatgaa aatttatgtc	240
atttgaggaa tcggcacgag caggctgccg ctccgccttc tgtcaaagcc tgaaatcacc	300
gtgttccagc ttgaatccat ttaatcttgc ccggtccttt ggctcaaaaac aaaaggcatc	360
tgcatacatt aagtaaaaac attcccgctc catttcatcc aatcccatca aaaaaacgga	420
acttcctcag cctcttccgt ctatatatta gcagcggaaa aggctctctt ttcgttttg	480
aaaaggagat gtgttgatata ttg ctg atg tac caa gtc aaa ccc gga gga acc	533
Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr	
1 5 10	

ctt gaa agc atc gcc gcc gat ttc aga acg acc cgg cag gcg ttg ctg	581
Leu Glu Ser Ile Ala Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu	
15 20 25	

cag gcg aat cct ggc tta aac ggc ggc caa gtg tcc gcg ggc cag tcg	629
Gln Ala Asn Pro Gly Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser	
30 35 40	

att atc att ccc ggc atc aga aat ccg gac aca att cca tac cgg att	677
Ile Ile Ile Pro Gly Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile	
45 50 55	

gcc gtg tct ctc aac gga aga acg ctc aga ttg tat gag cga gac aga	725
Ala Val Ser Leu Asn Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg	
60 65 70 75	

ctt gta aaa aca tat ccg att gcc gtc gga aaa atc ctc aca cag acg	773
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10295.204.ST25.txt

Leu Val Lys Thr Tyr Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr
 80 85 90

ccg aga ggc gaa ttt gtc atc gtc aac cgg cag cca aat ccg ggc ggc 821
 Pro Arg Gly Glu Phe Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly
 95 100 105

ccg ttc ggc gcc tac tgg ctg agc ctg tca aaa cag cac tac ggc atc 869
 Pro Phe Gly Ala Tyr Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile
 110 115 120

cat gga acg aat aac cct tcg tca att ggc aaa gct gtt tca agg gga 917
 His Gly Thr Asn Asn Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly
 125 130 135

tgt atc cgc atg cac aat cgg gat gtt ctg gaa ctt gct tct atc gta 965
 Cys Ile Arg Met His Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val
 140 145 150 155

ccc aac gga acc cga gtg tcc att aca cct tagacgagta catttccaga 1015
 Pro Asn Gly Thr Arg Val Ser Ile Thr Pro
 160 165

caaatgcaat ttgaaacaata caacatcttg tattaagata taatggacc tttaggtaa 1075
 ggagcgata tatggatctt tttaaaaatc gtaatttcgt ccgactttt ttcgcagctt 1135

tcgcttctca aatggaaacg acagtcgaa atatggctt cgcccttttc ttgctcgacc 1195

ggttcagcag ccagccggcc tatacgacaa tcgcccagct gatgtattcc ttgccgacgg 1255

tttcgtatt ctttatcgtc ggggtggctcg ctgaccgttt tgaccgcaag aaagtgcgg 1315

aaaactgtga ttggatcaga 'ggcgggactg actgtcgttc ttttcttgt attgtatctt 1375

caaattatac cgcttgtgtt tttagtccta tttatcagaa gcgcggttac aaaattttc 1435

taccggccg aagcaagttt ggtccaggcc attttaagaa aggaccagta tgcaaaggct 1495

<210> 131
 <211> 165
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 131

Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr Leu Glu Ser Ile Ala
 1 5 10 15

Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu Gln Ala Asn Pro Gly
 20 25 30

Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser Ile Ile Ile Pro Gly
 35 40 45

Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile Ala Val Ser Leu Asn
 50 55 60

Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg Leu Val Lys Thr Tyr
 65 70 75 80

Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr Pro Arg Gly Glu Phe

85

10295.204.ST25.txt

90

95

Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly Pro Phe Gly Ala Tyr
 100 105 110

Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile His Gly Thr Asn Asn
 115 120 125

Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly Cys Ile Arg Met His
 130 135 140

Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val Pro Asn Gly Thr Arg
 145 150 155 160

Val Ser Ile Thr Pro
 165

<210> 132
 <211> 1897
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1397)

<400> 132
 tttccatcg ggtgcagttt tatacggagg ccaaaacggt catgaatgta ccaaagaccg 60
 tatttgtccc tcagcctaac gtagattccg cggtcatcg gctgacgctg aggaaagagc 120
 cggctgtggc cggtcaagat gctgccttt tctttcaagt cgtaaaagca agctttgcac 180
 agcgtcggaa aacgctttc aacaacctcg tcaacaatct gccgaatggc aaagagaata 240
 aatcaaaaat tgaaagagcg cttcaggatt cacatatcg cggaaaacga cgccggagagt 300
 cgcttagcat tgaagagttc gccgtcttat ctgaccgctt gagagaagtc cttctttat 360
 ggagggcttt ttttattgtat gccgggcttt aagcctgatc aggcttgc tccgttcacc 420
 acttgaaggg cagggcacata ggctaaagaa gcaccttac ttttcgttg cttgatgttc 480
 atcaggatgg ggcttagtct atg tgt gga gtg aaa agc atg caa ttt aaa ata 533
 Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile
 1 5 10

gac gat atg gtc gtc aga aaa tct tat cga aga gat att tta ttt cga 581
 Gly Asp Met Val Val Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg
 15 20 25

att ata aga att gat caa tcg gca aat gga gaa cct gta gcc gtt ttg 629
 Ile Ile Arg Ile Asp Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu
 30 35 40

cac gga gat gag gtc aga tta atc gct gac gcg cat ttg ggg gat ctt 677
 His Gly Asp Glu Val Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu
 45 50 55

gag att gtc cgc gag gct gag tgg cag atg aga aag cgg gaa gaa gaa 725
 Glu Ile Val Arg Glu Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu

10295.204.ST25.txt

60	65	70	75	
acg aga atg aag gaa tcc ctc gat ctt ctc cgc cag gat tac aaa ctc Thr Arg Met Lys Glu Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu			80	773
			85	90
ctt cac gat aaa cat gag tac cgc gcc aca aac caa tat aac aat caa Leu His Asp Lys His Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln			95	821
			100	105
cag cag tac ttt cat atg ccc gga aga gtc ctt cat tta gac ggg gat Gln Gln Tyr Phe His Met Pro Gly Arg Val Leu His Leu Asp Gly Asp			110	869
			115	120
tcg gct tat ttg aaa aag tgt ctg gcg ctc tac gaa aag atc ggg gtt Ser Ala Tyr Leu Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val			125	917
			130	135
cct gta tac ggc att cat tgc tat gaa aag aaa atg tca tca gtc atc Pro Val Tyr Gly Ile His Cys Tyr Glu Lys Met Ser Ser Val Ile			140	965
			145	150
gag gaa ctg atc gat gaa tac cgc ccg gat ctt ctc gtc att acc gga Glu Glu Leu Ile Asp Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly			160	1013
			165	170
cac gat gcc tat tct aag cag aag ggc gat att aac aat ctg gat gcc His Asp Ala Tyr Ser Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala			175	1061
			180	185
tac agg cat tca aaa gat ttt atc gaa acc gtt caa aaa gcg aga aga Tyr Arg His Ser Lys Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg			190	1109
			195	200
aaa att ccc cat ctt gat cag ctc gtc att ttt gcc ggc gca tgc cag Lys Ile Pro His Leu Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln			205	1157
			210	215
tcc cat ttt gaa tca ctg atc aga gcc ggt gca aat ttc gca agc tct Ser His Phe Glu Ser Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser			220	1205
			225	230
ccg tcc aga gtc aac atc cat gcg ctt gat ccg gtc tat ata gtc gca Pro Ser Arg Val Asn Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala			240	1253
			245	250
aaa atc agc ttc act ccg ttt atg gac cgc att aac gtc tgg gaa gtg Lys Ile Ser Phe Thr Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val			255	1301
			260	265
ctc aga aat acc ttg acg aga gaa aag ggg ctc gga ggt att gag acg Leu Arg Asn Thr Leu Thr Arg Glu Lys Gly Leu Gly Ile Glu Thr			270	1349
			275	280
cgg ggc gta ttg cgt att gga atg cca tat aaa aca aaa gca aac gat Arg Gly Val Leu Arg Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp			285	1397
			290	295
taaacgagcc cgccggatgg cgggtttttg ctatgcacac gaaatgtttt tacttttt ttaaaaacat acataatgaa acgaaaaatg aggaaaataa gggaaaagtgc gcgtataatt				1457
tgtcacaaat attttattga cagaggctta tgaacgttga tataatttaa attttatttg acaaaaaatgg gcttctggtg tataactgaat atatgtgaggt ggatgcaatg gcgaaaaacgt				1517
tgtccgatat taaaagatcg cttgatggac atttggaaaa aaggctgacg ttaaaagcaa				1577
				1637
				1697

10295.204.ST25.txt
 acgggtggccg ccgaaaaacg attgagcggtt cgggcatttt agctgagacg tacccttctg 1757
 ttttgtat acaactagac caagacgaga attcgaaaatga aagagtttca tacagttatg 1817
 cggatattct tactgagacg gttgaattga gttttccga tgataaaacc agctcagtag 1877
 cccttaata agcagtggac 1897

<210> 133
 <211> 299
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 133

Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile Gly Asp Met Val Val
 1 5 10 15

Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg Ile Ile Arg Ile Asp
 20 25 30

Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu His Gly Asp Glu Val
 35 40 45

Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu Glu Ile Val Arg Glu
 50 55 60

Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu Thr Arg Met Lys Glu
 65 70 75 80

Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu Leu His Asp Lys His
 85 90 95

Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln Gln Gln Tyr Phe His
 100 105 110

Met Pro Gly Arg Val Leu His Leu Asp Gly Asp Ser Ala Tyr Leu Lys
 115 120 125

Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val Pro Val Tyr Gly Ile
 130 135 140

His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile Glu Glu Leu Ile Asp
 145 150 155 160

Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly His Asp Ala Tyr Ser
 165 170 175

Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala Tyr Arg His Ser Lys
 180 185 190

Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg Lys Ile Pro His Leu
 195 200 205

10295.204.ST25.txt

Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln Ser His Phe Glu Ser
 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295

Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser Pro Ser Arg Val Asn
 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295

Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala Lys Ile Ser Phe Thr
 245 250 255 260 265 270 275 280 285 290 295

Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val Leu Arg Asn Thr Leu
 260 265 270 275 280 285 290 295

Thr Arg Glu Lys Gly Leu Gly Ile Glu Thr Arg Gly Val Leu Arg
 275 280 285 290 295

Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp
 290 295

<210> 134
 <211> 1010
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(734)

<400> 134	60
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ttataaaaaa tcccggtttt tttgcttata ttgcggaaaa aatgggtgaaa atgaaaacaa	180
gctggagggtg attcaacatg aaaaagcga aaaggcgaac atttgaagaa cttgtctcg	240
aaaataaaaaa ggagctcatg accaaccagg agtttcttga tcggctggaa gataagcttg	300
aagagaaatt taagctgaag tgagtttta aaaatcgatt catgtttacg ctcccttttg	360
agaatcctaa tgctgaaaag gagggataga catgccgaga gaacacgaca aacagtctaa	420
atttgccccg agccatcttg ggacaaaacc ggtagaatat aagcgcaca aaggaaaaaa	480
gatgcatgat aaatcaggag aaacaccgat cattatgcag acaaaaggcg agtaaagatg	533
aaaaggaggc agagacccga atg aca cat caa aaa cat cat ccg gat gac aga	581
Met Thr His Gln Lys His His Pro Asp Asp Arg	
1 5 10	
tca gac aac gta gaa aag ctt caa gac atg gtg cag aac aca atc gaa	629
Ser Asp Asn Val Glu Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu	
15 20 25	
aac att gag gag tct gaa gag cag ctg tct ttt gcc agc gag gcg gaa	677
Asn Ile Glu Glu Ser Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu	
30 35 40	
cag gaa cag atc cgc gaa aaa aat gaa cgc cga aat gaa agc att gag	725
Gln Glu Gln Ile Arg Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu	
45 50 55	
gcg atg cgc aat gaa atc cat gac gag gcg gaa gcc cgc aaa aac gga	

10295.204.ST25.txt

Ala Met Arg Asn Glu Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly
60 65 70 75

tat cat caa taaaccaggg cgacctgggtt tttttgcatt aagcccgatcc
Tyr His Gln 774

gtcgtgtttt tgcccattgt atatgctaga attggattaa atacatttgt ggaaaaggga 834
gtagagggga aatttgtacg tctcaaaaaa agaaatagaa gtccgctatg ccgaaacaga 894
cccaaaatgg ggtgtcgct atcacgccaa ttatttgatt ttgggatggg aggttaagccc 954
qqacqqcttt aattaaagaa ctcggctttt ctatgccg aaatgggaga aagacg 1010

<210> 135
<211> 78
<212> PRT
<213> *Bacillus licheniformis*

<400> 135

Met Thr His Gln Lys His His Pro Asp Asp Arg Ser Asp Asn Val Glu
1 5 10 15

Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu Asn Ile Glu Glu Ser
20 25 30

Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu Gln Glu Gln Ile Arg
35 40 45

Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu Ala Met Arg Asn Glu
50 . 55 . 60

Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly Tyr His Gln
65 70 75

<210> 136
<211> 2407
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1907)

<400> 136
gcatactgta aaaggccggg tgaatgaaga gcttttggaaa tcggtcgtga tagatccaaa 60
tggcgaattt tatgttatgcg gtccgccttc atttatgaaa agcgtgattt aaggatttgc 120
aaaccttggc gtttcgatgg aaaacatccg ctatgagagc tttgcttcat ctcttgatat 180
gcaaatacg aactaacctc aagaaggcag ctgtcaaacc gacagctgcc tcagcgtgtc 240
gacaaaccct cgcattgcgtt gtcagtcctg cgcgtcggtg ctcacgaatt ccaacattcg 300
ctccgcctcg atgctcggcc ttcccttagact gcaagggttt tcaatcacgc tgaaagaagg 360
atqacaaaat cccaaaacta agagctgttt tggttttttgc tcagcaatct aaggcagctg 420

10295.204.ST25.txt

tcaatccgac agctgccttt catctttca aaaccggct catacaataa agagaagtcc	480
aaccgggggg gattttagta ttg agc ata cgg gag caa aaa gag ctg cag cgg Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg 1 5 10	533
gcg att gaa gaa att acg gaa atc gcg gaa gga ttc ggc ctt gat ttt Ala Ile Glu Glu Ile Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe 15 20 25	581
tac ccg atg aga tat gag att tgt cct gct gaa att att tat aca ttc Tyr Pro Met Arg Tyr Glu Ile Cys Pro Ala Glu Ile Tyr Thr Phe 30 35 40	629
ggt gca tac ggg atg ccg aca aga tac agc cat tgg agt ttc gga aag Gly Ala Tyr Gly Met Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys 45 50 55	677
caa ttt cac aaa atg aag ctt cac tat gac ttt ggc ttg agc aaa ata Gln Phe His Lys Met Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile 60 65 70 75	725
tat gag ctt gtc att aat tca gat ccg tgt tat gcg ttt ttg ctg gac Tyr Glu Leu Val Ile Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp 80 85 90	773
agc aat tca ttg att caa aat aag ctg att gtc gca cac gtc ctt gct Ser Asn Ser Leu Ile Gln Asn Lys Leu Ile Val Ala His Val Leu Ala 95 100 105	821
cat tgt gat ttc ttt aaa aat aac tgc cgt ttt caa aat acg aag cgc His Cys Asp Phe Phe Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg 110 115 120	869
gat atg gtt gaa agc atg tcg gcg aca gca gag cgg att aaa cat tat Asp Met Val Glu Ser Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr 125 130 135	917
gaa acg gta cac ggt tca aaa gaa gtc gaa gca ttt ctc gat gcg gtg Glu Thr Val His Gly Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val 140 145 150 155	965
ctg gcg att gaa gaa cac att gac cct tcg ctc gtg agg ccg aag ctg Leu Ala Ile Glu Glu His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu 160 165 170	1013
tcg tgg agc gta gat gat gaa gag gaa gaa acc ggc gcg ccg gcc Ser Trp Ser Val Asp Asp Glu Glu Glu Glu Thr Gly Ala Pro Ala 175 180 185	1061
act cct tat gac gac ctc tgg gaa ctg gat cat aaa gga tcg aaa gag Thr Pro Tyr Asp Asp Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu 190 195 200	1109
aag aag aaa agg acg aaa aaa aag ttt ccg ccg aaa ccg gaa aaa gac Lys Lys Arg Thr Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp 205 210 215	1157
att ctg ctg ttc ata gaa gag cat tcg cgg gag ctg gag cct tgg cag Ile Leu Leu Phe Ile Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln 220 225 230 235	1205
cgc gat att tta acg atg atg aga gag gaa atg ctg tat ttc tgg ccg Arg Asp Ile Leu Thr Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro 240 245 250	1253
cag ctt gaa acg aaa atc atg aat gaa ggc tgg gcg tcc tat tgg cat Gln Leu Glu Thr Lys Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His	1301

255	10295.204.ST25.txt	265	
260		265	
cag cga atc atc cgt gag ctt gat ctg aca tca agt gaa gcg atc gaa Gln Arg Ile Ile Arg Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu 270 275 280			1349
ttc gcc aag ctg aac gcg gga gtg gtt cag ccg tcc aaa acg gga atc Phe Ala Lys Leu Asn Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile 285 290 295			1397
aat cct tat tat ctc gga ttg aaa ata ttt gag gac ata gag gag cgc Asn Pro Tyr Tyr Leu Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg 300 305 310 315			1445
tac aac aac ccg aca gaa gac atg aaa aag atg ggg gta gag ccg aac Tyr Asn Asn Pro Thr Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn 320 325 330			1493
tct ggg aga gaa aaa ata ttt gaa gtc agg gag atc gaa tca gac att Ser Gly Arg Glu Lys Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile 335 340 345			1541
tca ttt atc agg aac tat tta acg aag gat ctt gtg atg cgg gaa gac Ser Phe Ile Arg Asn Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp 350 355 360			1589
ctc tac ttg ttt caa aaa cag gga agg gat tat aaa atc gtc gac aag Leu Tyr Leu Phe Gln Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys 365 370 375			1637
gat tgg gag gct gtg cgc gat cag ctt gtc agc atg aga gtc aac gga Asp Trp Glu Ala Val Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly 380 385 390 395			1685
gga ttt cct tat ttg aca gtt gag gac gga gat tac tta aag aac aat Gly Phe Pro Tyr Leu Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn 400 405 410			1733
gaa tta tac atc aag cat tgg tat gaa ggg atc gaa ctc gat ttg aag Glu Leu Tyr Ile Lys His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys 415 420 425			1781
tat ctt gaa aaa gtt ctg cct tac ctc cac cag cta tgg gga aga agc Tyr Leu Glu Lys Val Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser 430 435 440			1829
gtg cat gtc gag acc gtg ctc gaa gat aaa ccc gtc atg ttt tcc tat Val His Val Glu Thr Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr 445 450 455			1877
gat gga aag gct gtc cac cgc aga tat tta taaaggctgc attttggcag Asp Gly Lys Ala Val His Arg Arg Tyr Leu 460 465			1927
ccttttttct tttaaagcgc aacgatttca actcgccgt cctttcaaaa gaaatgccaa			1987
attaatgcac gtttgcgcag tttagact tcattataaa aatgtaaaaat aaagtattta			2047
atgatatttc taaaattgtt attttagctg ccggaaagcg taaaaatgtt gtatttaagt			2107
tacctttgaa atgtttatgtt aatattatct accctttaaa acttttttg aaaacgaata			2167
attaaggaaat ttgacatagt aagtcaagac tatacctgat ggaattccct ccttataata			2227
gaagcagagg aaggcgttgc tcaaaaaat gaaactgcta attttcgcct			2287
ttgaaaaatataatattct gctattggaa ggacaacatg aaaaaacaag taataacagc			2347

10295.204.ST25.txt

agcatcagcg gttgttttag gatcgactt gtttgcggga gccgcttccg cgcaaaccat 2407

<210> 137

<211> 469

<212> PRT

<213> *Bacillus licheniformis*

<400> 137

Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg Ala Ile Glu Glu Ile
1 5 10 15Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe Tyr Pro Met Arg Tyr
20 25 30Glu Ile Cys Pro Ala Glu Ile Tyr Thr Phe Gly Ala Tyr Gly Met
35 40 45Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys Gln Phe His Lys Met
50 55 60Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile Tyr Glu Leu Val Ile
65 70 75 80Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp Ser Asn Ser Leu Ile
85 90 95Gln Asn Lys Leu Ile Val Ala His Val Leu Ala His Cys Asp Phe Phe
100 105 110Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg Asp Met Val Glu Ser
115 120 125Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr Glu Thr Val His Gly
130 135 140Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val Leu Ala Ile Glu Glu
145 150 155 160His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu Ser Trp Ser Val Asp
165 170 175Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala Thr Pro Tyr Asp Asp
180 185 190Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu Lys Lys Arg Thr
195 200 205Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp Ile Leu Leu Phe Ile
210 215 220Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln Arg Asp Ile Leu Thr
225 230 235 240

10295.204.ST25.txt

Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro Gln Leu Glu Thr Lys
245 250 255

Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His Gln Arg Ile Ile Arg
260 265 270

Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu Phe Ala Lys Leu Asn
275 280 285

Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile Asn Pro Tyr Tyr Leu
290 295 300

Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg Tyr Asn Asn Pro Thr
305 310 315 320

Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn Ser Gly Arg Glu Lys
325 330 335

Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile Ser Phe Ile Arg Asn
340 345 350

Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp Leu Tyr Leu Phe Gln
355 360 365

Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys Asp Trp Glu Ala Val
370 375 380

Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly Gly Phe Pro Tyr Leu
385 390 395 400

Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn Glu Leu Tyr Ile Lys
405 410 415

His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys Tyr Leu Glu Lys Val
420 425 430

Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser Val His Val Glu Thr
435 440 445

Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr Asp Gly Lys Ala Val
450 455 460

His Arg Arg Tyr Leu
465

<210> 138
<211> 1291
<212> DNA
<213> Bacillus licheniformis

10295.204.ST25.txt

<210> 139
<211> 97

10295.204.ST25.txt

<212> PRT
 <213> *Bacillus licheniformis*

<400> 139

Val Glu Val Thr Asp Val Arg Leu Arg Arg Val Asn Thr Asp Gly Arg
 1 5 10 15

Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His Glu Phe Val Val His
 20 25 30

Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu Phe Val Ala Met Pro
 35 40 45

Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp Ile Ala His Pro Ile
 50 55 60

Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala Val Leu Asn Glu Tyr
 65 70 75 80

His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr Glu Glu Ile Gly Ala
 85 90 95

Ser

<210> 140
 <211> 1694
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1451)

<400> 140	60
gctcgagggg gatgcgcttt cgtcaaccct taaaaacgcc cgatatctgc cgaaatggct	60
gaagctgcaa aaggaaattt aacaagagat tgaaaaagcg atcaaatcga atcagcgcga	120
aacgctgatt gatgccatca accaaaaat taaaaaatac aaccccacct gtccgaacca	180
attccaaaaa ggccttgttt cagccaaaaa cctcgaaagt cagctcaaattt attggagctg	240
atgccattcc ctgcacttat tcataaaaat aattgccaat aacaatcatc ttatgtaaaa	300
taaaggtaat atttatgctt taaaaaagga gaaaggatga atgaagaagt ggaagcggaa	360
gcggcatacg aaaaagcggc ctggctcctg aatcagtggt acaccatgat caagcgcct	420
gaagcgctcc aggctgtatc tttgaggtac gagatccaaa acctgcttc taaaatggag	480
aaaagcggag atctggagct ttg ttt tca gct gtt gga cta tcg ctg caa att	533
Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile	
1 5 10	
gat gat gga gca gtt tca gaa tca gcc gag ctt ttc cgg aaa att aaa	581
Asp Asp Gly Ala Val Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys	
15 20 25	

10295.204.ST25.txt

agg cag aag gaa acg gtt aag agc gcg gat gac atc att cag tac tat Arg Gln Lys Glu Thr Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr 30 35 40	629
ttt ttc ttt ttt tca ggc atg tat gag ttt tat gag aaa aac tat ttt Phe Phe Phe Ser Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe 45 50 55	677
gag gcg atc agc tgt tac aag aaa gcg gaa gcg aag ctg cat aaa ctg Glu Ala Ile Ser Cys Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu 60 65 70 75	725
acc gat gaa att gaa aaa gcg gaa ttt tat tat aaa atc gcg acc gcc Thr Asp Glu Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala 80 85 90	773
tac tac caa ata gac gat cat ttc aga tcg ttg aac tac tcc gaa aaa Tyr Tyr Gln Ile Asp Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys 95 100 105	821
gcf ctc tca ctt ttc agc aag cat aaa gaa tac ata gac aaa acg atc Ala Leu Ser Leu Phe Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile 110 115 120	869
gga tgc gaa atg ata ctc gga tcg gtg cag ttt gaa ttg ttc cgc atc Gly Cys Glu Met Ile Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile 125 130 135	917
aaa caa gct gag gag cac tac ggg cgg gcg ctt gat cag gcc gtt gcc Lys Gln Ala Glu Glu His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala 140 145 150 155	965
ctt caa aac cgg cga atc atc ggg ctg atc tat cat aat atg gga ctg Leu Gln Asn Arg Arg Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu 160 165 170	1013
aac tat gcc aaa tgc ggc atg ccg ctt ttg gcg gag gag cac ttt aga Asn Tyr Ala Lys Cys Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg 175 180 185	1061
aaa gcc ctt tca atc ggt gtc cat gag caa tcg gtt ttt ggc att aac Lys Ala Leu Ser Ile Gly Val His Glu Gln Ser Val Phe Gly Ile Asn 190 195 200	1109
acc ctt ttc gag ctg tct cac ctc atg tac aaa aac ggt tct ccc gaa Thr Leu Phe Glu Leu Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu 205 210 215	1157
gaa gcg aga cgt ctc tgc aaa gag gga ttt acc aga tcg gcc gaa tta Glu Ala Arg Arg Leu Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu 220 225 230 235	1205
gga gag gat gaa tac gca gcg aag ttc agg ctg att ttc gcc ctg tat Gly Glu Asp Glu Tyr Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr 240 245 250	1253
gac gct ggc cat ccg ctc gat att gaa ttt tcg ctt gaa tat atg agt Asp Ala Gly His Pro Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser 255 260 265	1301
gat aaa cgg cta tgg ccg cat gtt gct gaa ctg aca aaa gat att gcc Asp Lys Arg Leu Trp Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala 270 275 280	1349
gac tat tac atg aag tca ggc gac cat gaa aaa agc gcg ctt tac ctg Asp Tyr Tyr Met Lys Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu 285 290 295	1397

10295.204.ST25.txt

gaa aaa tcg cag cat gcg aaa aat caa ata tat aaa atg aag gag ggg
 Glu Lys Ser Gln His Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly
 300 305 310 315

1445

att ata tgaaaaaaaaa catttgtttt ttccgcgtca tgcttgttt cctgatgggg
 Ile Ile

1501

ggaagcttca cagctgattc tgcagcacag gacggatcg ttcagccatt gggaaagtgc
 gtgtttcctg ccagcggacg atagagataa cttgccgaga tagaaatggc ctcccgtctt
 ttgctatcat cgtctcacct gaaggcaatt gaaggagca gtagtgatgc cgataaaaga
 gatttcgcgc tgc

1561

1621

1681

1694

<210> 141
 <211> 317
 <212> PRT
 <213> *Bacillus licheniformis*

<400> 141

Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile Asp Asp Gly Ala Val
 1 5 10 15

Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys Arg Gln Lys Glu Thr
 20 25 30

Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr Phe Phe Phe Ser
 35 40 45

Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe Glu Ala Ile Ser Cys
 50 55 60

Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu Thr Asp Glu Ile Glu
 65 70 75 80

Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala Tyr Tyr Gln Ile Asp
 85 90 95

Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys Ala Leu Ser Leu Phe
 100 105 110

Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile Gly Cys Glu Met Ile
 115 120 125

Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile Lys Gln Ala Glu Glu
 130 135 140

His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala Leu Gln Asn Arg Arg
 145 150 155 160

Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu Asn Tyr Ala Lys Cys
 165 170 175

10295.204.ST25.txt

Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg Lys Ala Leu Ser Ile
180 185 190

Gly Val His Glu Gln Ser Val Phe Gly Ile Asn Thr Leu Phe Glu Leu
195 200 205

Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu Glu Ala Arg Arg Leu
210 215 220

Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu Gly Glu Asp Glu Tyr
225 230 235 240

Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr Asp Ala Gly His Pro
245 250 255

Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser Asp Lys Arg Leu Trp
260 265 270

Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala Asp Tyr Tyr Met Lys
275 280 285

Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu Glu Lys Ser Gln His
290 295 300

Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly Ile Ile
305 310 315

<210> 142
<211> 1260
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1244)

<400> 142	60
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cggccctcgg caccattgat cacacacatg ccggtgtggc ggaattggca gacgcgcacg	120
actcaaaatc gtttccttc gggagtgtcg gttcgacccc gaccaccggt atcactaaac	180
atcgattgc caaacatgaa aagagcgttc ctacaaaagg agcgctctt ttatattttc	240
cttatcttgg aacgaagccg taagaatttt ttcttaagga ctgcgagctc cggaagctac	300
ggaaacatac cgtgagattt atcgaaatga gcttaatacg gtgcagaaac ttttacaaaa	360
gcaaaaatat atctgatgat ttattatcta ttatagggc gaaaagtaaa ttattgatac	420
aaacttcttt gcaaagattt gtaactttct gtaaatgtt ctcatagcga tagaggcagt	480
aaagtgtggg aggttgaca atg aaa gca gca gcc tct gtg aac gta gcc aat	533
Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn	
1 5 10	

ctc atc aat cag tgg tat gtt cac ata aaa aag aga gat gtt tca aat 581

10295.204.ST25.txt

Leu Ile Asn Gln Trp Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn
 15 20 25

gcc gta gaa ctt agg gac aga ata aaa ggc ctt tta aac gta atg gaa 629
 Ala Val Glu Leu Arg Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu
 30 35 40

gaa gat cag gat gtt ttg ctt tac ttt aat cta ctt gat tac agg ttc 677
 Glu Asp Gln Asp Val Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe
 45 50 55

aga gta tta atg gaa gac gtc gcg ggg gag ccg cag ctt ccg cct att 725
 Arg Val Leu Met Glu Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile
 60 65 70 75

gct gaa gat aag gcg aag aca gac ggt ttg tta cga tac tat tac ttt 773
 Ala Glu Asp Lys Ala Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe
 80 85 90

ctc ttt aaa gga atg tat gaa agt gcg agg agc aac tac tct aaa gcg 821
 Leu Phe Lys Gly Met Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala
 95 100 105

ctt aat tgt ttt aga gtt gcc gag cgg cag ctc gat aat gtc gaa gat 869
 Leu Asn Cys Phe Arg Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp
 110 115 120

gaa atc gaa aag gcc gag ttt cat tat aag ctt gga aat ctc tat tat 917
 Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr
 125 130 135

ttt acg aaa aca act cta ctt tct ttt cat cat ctt tca atc gcg aag 965
 Phe Thr Lys Thr Thr Leu Leu Ser Phe His His Leu Ser Ile Ala Lys
 140 145 150 155

agc att tat agg gct tat gaa gaa tat aag aca cag tcg ata aac tgt 1013
 Ser Ile Tyr Arg Ala Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys
 160 165 170

acg gtg ctg ctc gca ctc aat tat ata gac gac gga cgt tta aca aga 1061
 Thr Val Leu Leu Ala Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg
 175 180 185

gct gaa aat atg ctt aag agt tgc gca gaa aga ctg atc aag atg ggc 1109
 Ala Glu Asn Met Leu Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly
 190 195 200

gat aat cat ctg ctg gcg gct gtc tac tat gat ctc ggc ttt tta aaa 1157
 Asp Asn His Leu Leu Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys
 205 210 215

att caa gag gat aaa cat gaa gaa gca ctc gag tat ttc gac ctc tca 1205
 Ile Gln Glu Asp Lys His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser
 220 225 230 235

ttt aaa acg ggt gat atc gaa aaa aat gag ccg ggg act tagctcgata 1254
 Phe Lys Thr Gly Asp Ile Glu Lys Asn Glu Pro Gly Thr
 240 245

gatgta 1260

<210> 143
<211> 248
<212> PRT
<213> Bacillus licheniformis

<400> 143

10295.204.ST25.txt

Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn Leu Ile Asn Gln Trp
1 5 10 15

Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn Ala Val Glu Leu Arg
20 25 30

Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu Glu Asp Gln Asp Val
35 40 45

Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe Arg Val Leu Met Glu
50 55 60

Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile Ala Glu Asp Lys Ala
65 70 75 80

Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Phe Leu Phe Lys Gly Met
85 90 95

Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala Leu Asn Cys Phe Arg
100 105 110

Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp Glu Ile Glu Lys Ala
115 120 125

Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr Phe Thr Lys Thr Thr
130 135 140

Leu Leu Ser Phe His His Leu Ser Ile Ala Lys Ser Ile Tyr Arg Ala
145 150 155 160

Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys Thr Val Leu Ala
165 170 175

Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg Ala Glu Asn Met Leu
180 185 190

Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly Asp Asn His Leu Leu
195 200 205

Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys Ile Gln Glu Asp Lys
210 215 220

His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser Phe Lys Thr Gly Asp
225 230 235 240

Ile Glu Lys Asn Glu Pro Gly Thr
245

<210> 144
<211> 2119
<212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1619)

<400> 144	tacgcagtcg aaatgaacccg tcttatcaag ttcgagatgg aagggtctat tggttaaccc	60	
	ttgatactaa aggggtgat cagacttcga tttgattgca cccgaataaa ctttatgttt	120	
	gtgtaccgca gatataatct attgcctatc gatTTTctaa aaggcgtaga aatgtatctg	180	
	cggTTTTc ttttagcttt tatttctaaa aagaggTTTg aattttgcTT cctaacgatt	240	
	agttatgcc aattacatat caacaggaaa atataatcct tcattctgttc tgccttcTT	300	
	cctataactc taaaattcac ccaaacacgg aaaacgaatc atattgatta ggccaaaaaa	360	
	cctctaactt ataaaagattt ctgagaatgt tgTTgtgaaa aattattact tttatgtaaa	420	
	atgatgacta tgaataaaaaa gggaaattgct atttgggTT ttttagaaaaa ttataatctt	480	
	gcgagaaagg aagaggatAT gtg agc gtg ata cca tat gat ttg gtt gcg acg	533	
	Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr		
1	5	10	
	aaa atg aat ttt tgg tat aca gcc tta. aaa aac aat tgg aca ggc aag	581	
Lys Met Asn Phe Trp Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys			
15	20	25	
gct gag gat act aag aaa gaa gtt gaa cga gaa tta gaa caa atg gaa	629		
Ala Glu Asp Thr Lys Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu			
30	35	40	
caa aat cag gat gtg att gtc tat tac aac tta ctg ctc ttc cgg cat	677		
Gln Asn Gln Asp Val Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His			
45	50	55	
aat ctt caa ctt gat tat atg tat tct aaa ccc ggt gta aat tta aat	725		
Asn Leu Gln Leu Asp Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn			
60	65	70	75
agt cgt ttt gat gag ttc aaa aag att cgc gat cag aat aat ctg gaa	773		
Ser Arg Phe Asp Glu Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu			
80	85	90	
gga atg ttg gat tat tat cat ttt ttc gct gga atg tat cat ttc	821		
Gly Met Leu Asp Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe			
95	100	105	
aga caa aaa gaa tta atc ctt gcg ctg aat ttt tat agg gat gcc gag	869		
Arg Gln Lys Glu Leu Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu			
110	115	120	
aaa aaa ctc gat tct ttt gat tgt gat gaa ctg gaa aag gct gaa ttt	917		
Lys Lys Leu Asp Ser Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe			
125	130	135	
tat ttc aag gca tct gaa gtg tat tac cat atg aaa caa acc atc ttt	965		
Tyr Phe Lys Ala Ser Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe			
140	145	150	155
tcg atg aat tat gca agt cgt gcg tat aac tta ttc aaa aag tat gat	1013		
Ser Met Asn Tyr Ala Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp			
160	165	170	

10295.204.ST25.txt

act tac ggt gag cgt cga gta caa agt cag ttt att att gca ggt aac Thr Tyr Gly Glu Arg Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn 175 180 185	1061
tgg cta gat cat atg tat ccc gaa aaa gct cta cat aat tta aat aaa Trp Leu Asp His Met Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys 190 195 200	1109
gag ctt aaa gag tca gag aca caa gga att ctt cat ctt atg ggt tca Glu Leu Lys Glu Ser Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser 205 210 215	1157
tca cat tta aat atc gga ata tgc tac aat aaa ttg gaa gat gtc gat Ser His Leu Asn Ile Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp 220 225 230 235	1205
aaa gca acc tac aat ttt caa aga gct ctg aac ctt tat aaa gag gag Lys Ala Thr Tyr Asn Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu 240 245 250	1253
aag cat agt ttt ttg cca aaa aca tta ttc aac ctc gca cat gtc agg Lys His Ser Phe Leu Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg 255 260 265	1301
gca aag caa ggg aag ttg tca ata act gat gac cta tac tat gaa ggc Ala Lys Gln Gly Lys Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly 270 275 280	1349
aaa gag ttg gct gaa aag aac aag aat tta gat atg ctt gca aag ttt Lys Glu Leu Ala Glu Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe 285 290 295	1397
gat tta ata aaa ggg ctt tat ctt tca ttt gat ctg gat atg gtt cgc Asp Leu Ile Lys Gly Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg 300 305 310 315	1445
gaa tcg ttc aag ttt ttc gaa agt aaa ggc aag tat gca gac atg gag Glu Ser Phe Lys Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu 320 325 330	1493
gaa tac ggt ctt ata gcg gct gaa cta tta gag aaa aaa gaa aaa att Glu Tyr Gly Leu Ile Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile 335 340 345	1541
cga gat gca gtg gaa ttc tac cggtataca gtt aat gcg aga aga caa Arg Asp Ala Val Glu Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln 350 355 360	1589
att caa agg agt gct ttt cta cat gta aac taaatcggttc taggggtagt Ile Gln Arg Ser Ala Phe Leu His Val Asn 365 370	1639
taaaggcagca ggatttctta ctataaaaaa gaatttcccc cagcattatt aaaaccta attttgatta cttgattatt attttaagta atcgcagaaa gaaaggctgg tctatggcaa gctatttaaa atccagaatc gtatcttatac tgtttattct tttggaaatg gggaccggat tcgcaatttg cgaggtgtca atggaaaatc cgaattactc cttagcttgc gcggcttt tcataggttt tacgattggg gaatgcttca tgattagaaa atggtaaatt ttgatcatga cgggataactc tttaccctct tctataaaag tgggacagac agttgaaaag ccggtaaatt catagccttg tatttcaaca gtaacttctt ctatatcggtt gtttcatttt ttcatttt cttaatacat taaatcacct ctttatataca gtatgttcc attaaagaag aacaggatct	1699 1759 1819 1879 1939 1999 2059 2119

10295.204.ST25.txt

<210> 145

<211> 373

<212> PRT

<213> *Bacillus licheniformis*

<400> 145

Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr Lys Met Asn Phe Trp
1 5 10 15

Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys Ala Glu Asp Thr Lys
20 25 30

Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu Gln Asn Gln Asp Val
35 40 45

Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His Asn Leu Gln Leu Asp
50 55 60

Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn Ser Arg Phe Asp Glu
65 70 75 80

Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu Gly Met Leu Asp Tyr
85 90 95

Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe Arg Gln Lys Glu Leu
100 105 110

Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu Lys Lys Leu Asp Ser
115 120 125

Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe Tyr Phe Lys Ala Ser
130 135 140

Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe Ser Met Asn Tyr Ala
145 150 155 160

Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp Thr Tyr Gly Glu Arg
165 170 175

Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn Trp Leu Asp His Met
180 185 190

Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys Glu Leu Lys Glu Ser
195 200 205

Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser Ser His Leu Asn Ile
210 215 220

Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp Lys Ala Thr Tyr Asn
225 230 235 240

10295.204.ST25.txt

Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu Lys His Ser Phe Leu
 245 250 255

Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg Ala Lys Gln Gly Lys
 260 265 270

Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly Lys Glu Leu Ala Glu
 275 280 285

Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe Asp Leu Ile Lys Gly
 290 295 300

Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg Glu Ser Phe Lys Phe
 305 310 315 320

Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu Glu Tyr Gly Leu Ile
 325 330 335

Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile Arg Asp Ala Val Glu
 340 345 350

Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln Ile Gln Arg Ser Ala
 355 360 365

Phe Leu His Val Asn
 370

<210> 146
 <211> 1405
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(905)

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gttaaaacag gtgaaggggaa aagattccac tagagtggat gctggtcaat ttttataact		180
ctttatTTTA aaagggtttc gaggagctgt ggaagcttt gcaggcatca ataaaagatc		240
aatatTTTCT ttaagttgat cattcacaaa tcgaattact tctttattag gccaaGTTTC		300
atTTTcatgg atgcacaggg ttatCCGCA aattCCTTCa aatagtaaac CCTTcaagat		360
cgcggTggac gaaatttccc ttcgagaata ctgcaggTgc ggcttggaaa agagcatata		420
gagattcagg cgtcttagca ggcgtttt tgTTgctgat ttTattgcgg cataccgaaa		480
atTTTTcac ttTcaacctt attatCACCC gaattatagt aatatTTTA caaaaatgaa		533
ataaaaaaggt ataggcggaa gtg aaa cag tta ata ccc tcg tca aaa gtc gga		
Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly		
1 5 10		

gtg aaa atc cac gaa tgg tat aaa atg ata aga gag ttt agc gta ccg
 Page 209 581

10295.204.ST25.txt

val Lys Ile His Glu Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro			
15	20	25	
gat gca gag gct tta aaa gaa gaa gta gag aag gaa att aat caa atg			629
Asp Ala Glu Ala Leu Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met			
30	35	40	
gaa gaa gat cag gac tta ctc ctt tac tat cag ttg atg tgt ttt aga			677
Glu Glu Asp Gln Asp Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg			
45	50	55	
cat caa tta atg tta gaa tat tta gaa cct act aac aaa aga aaa caa			725
His Gln Leu Met Leu Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln			
60	65	70	75
gga caa tca ata aac aaa ttg ttg gcc caa atc gag gag cct cga aga			773
Gly Gln Ser Ile Asn Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg			
80	85	90	
gat tta aat ggc ctc ctt agt tac tac tca ttt ttc ttt agg ggc atg			821
Asp Leu Asn Gly Leu Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met			
95	100	105	
tat gaa ttt gag aaa aaa cag tac atc aaa gca ata gag ttt tat cga			869
Tyr Glu Phe Glu Lys Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg			
110	115	120	
aac gca gaa aaa cag ttg gct ctc att acg atg tta tagaacaagc			915
Asn Ala Glu Lys Gln Leu Ala Leu Ile Thr Met Leu			
125	130	135	
cgagttcac tttaaatgg ctgaagcata ctacatcatg aaacagacac atgtatcata			975
tattaaggc cttaataata tacaataatc atgaactcta cacagtccgt aaaatccaat			1035
gtttatttgt tatcgccgggt aactatgacg attaatgcg ccatgacaaa gccttacccc			1095
acctggaaaa tgcacttgaa ttagcgatag agatcgacaa taaaaggctc attagttctg			1155
cctattttaa tatagccac tgtcatgaat gtatggaga cattgatgca gcagttgaat			1215
atgctgaaaa agccgtagag attaatctaa aagaagaata taacaaccta ccacaatcat			1275
tatattactc tactcaactt cttaataagc agaaaaacta cgagcgcgca atcgagatat			1335
ttcttattgg ttagacaaac agctcgaaaa ttcaacgata ccctattcac ttctctat			1395
gaardatcttg			1405

<210> 147

<211> 135

<212> PRT

<213> *Bacillus licheniformis*

<400> 147

Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly Val Lys Ile His Glu
1 5 10 15Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro Asp Ala Glu Ala Leu
20 25 30Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met Glu Glu Asp Gln Asp
35 40 45

10295.204.ST25.txt

Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg His Gln Leu Met Leu
 50 55 60

Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln Gly Gln Ser Ile Asn
 65 70 75 80

Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg Asp Leu Asn Gly Leu
 85 90 95

Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met Tyr Glu Phe Glu Lys
 100 105 110

Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg Asn Ala Glu Lys Gln
 115 120 125

Leu Ala Leu Ile Thr Met Leu
 130 135

<210> 148
 <211> 2104
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (501)..(1604)

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gacgatatacg gctttttgat cgcgAACCCa gcgtccccca accattccgc tttgaatgcg	180
gtaatcgatg gtatggatcat tttaatgta gatttcatat tcccatccgt tttcatacgt	240
atagatcata tggcttccta caaactctt tacatcttga ttcatatgaa ccgctccctt	300
atttgttat tgtaatcgaa acatgttgat atttacatat ataattataa aatgccgtca	360
aaaaagatgt caaacgaaaa tacttcctga gagatttgca caaataaaga agattgttac	420
gattaatgtc agaattttga gttatcttag gaaattatgc caatatttag aaaagtgttac	480
gtcaaaaaat aagcgattct gtaaaatgaa aaacaaccca taaaaaggaa atgacatggg	533
aagaaaggaa ggataaacga ttg aag aca aaa att gcg tat gag gaa gtt gcg	581
Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala	
1 5 10	

gga atg ctt aat caa tgg tat gtc atg atc aag cgt cac gaa gta tca	581
Gly Met Leu Asn Gln Trp Tyr Val Met Ile Lys Arg His Glu Val Ser	
15 20 25	
caa gcg gtc tcg att aaa tgc gac att gag cac cag ctg ccg aat atg	629
Gln Ala Val Ser Ile Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met	
30 35 40	
gaa gaa aat caa gat ctg ctt ctt tat ttt aat ctt tta gac tat cgg	677
Glu Glu Asn Gln Asp Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg	
45 50 55	

10295.204.ST25.txt

cac aag ctg ctg aca gaa gag ttt gcc gct tcc aac aaa ctg ttc gag His Lys Leu Leu Thr Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu	725
60 65 70 75	
gat att cag gag caa aaa gcc gat atg caa agc aca gat gac atg att Asp Ile Gln Glu Gln Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile	773
80 85 90	
gaa tat tat tat ttc ttt ttc gct ggc atg tac gaa ttt cat aag aag Glu Tyr Tyr Tyr Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys	821
95 100 105	
gat tat aca aat gca atc aat tat tat aaa tta gcc gag gaa aag ctc Asp Tyr Thr Asn Ala Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu	869
110 115 120	
agg aca atc ccc gat caa atc gaa atc gcc gaa ttc cat tac aaa ctg Arg Thr Ile Pro Asp Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu	917
125 130 135	
gct atc gcc tac tat caa atc aaa caa aat ttc ctt tcc tta aac cat Ala Ile Ala Tyr Tyr Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His	965
140 145 150 155	
gcg aaa aca gct cta aaa acc ttc aaa gca cat gat gat tac att caa Ala Lys Thr Ala Leu Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln	1013
160 165 170	
aaa gcg atc agc aac gat atg ctg atc ggg gca aat aaa ctc gat tta Lys Ala Ile Ser Asn Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu	1061
175 180 185	
ttt cgt ttt gat gaa gcc gaa cag cat tac aag caa gcc ctt aaa gac Phe Arg Phe Asp Glu Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp	1109
190 195 200	
gcg gca ctg atc aaa cat cat gtc ctc ctc ggc atg gct cac cac aac Ala Ala Leu Ile Lys His His Val Leu Leu Gly Met Ala His His Asn	1157
205 210 215	
tta ggg ttg agc tat gtc aat cgc aac ctc ctc aca ttg gct gaa cat Leu Gly Leu Ser Tyr Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His	1205
220 225 230 235	
cat ttc aaa gaa gcg ctg ctt atc aaa gag cat gaa gaa tcg gtt tac His Phe Lys Glu Ala Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr	1253
240 245 250	
ggc atc cat tcc atg ttt gaa ctg aca cat gtg ctg tac aaa tca aat Gly Ile His Ser Met Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn	1301
255 260 265	
gtt gtc aaa gaa gca cgc aaa ttg tat gaa aaa gga ttt ttc cgt gcg Val Val Lys Glu Ala Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala	1349
270 275 280	
gaa aaa gca gga gaa agg gaa tat ttg tcg aaa ttt aaa ctt att cat Glu Lys Ala Gly Glu Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His	1397
285 290 295	
gct ctg tat gat gaa cag gat cca ctt acg gtt gaa cat gct tta gaa Ala Leu Tyr Asp Glu Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu	1445
300 305 310 315	
tat ctt aaa acg atc aat ctc tgg acg gat gta gcg gaa tta aca ttt Tyr Leu Lys Thr Ile Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe	1493
320 325 330	

10295.204.ST25.txt

gat atc gca ctt tac tat aaa gaa aat gga gat gca gac aaa gct gcc Asp Ile Ala Leu Tyr Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala 335 340 345	1541
gaa tat ttt gaa gaa tct cat cat gca aga gac caa att ctt aaa aga Glu Tyr Phe Glu Glu Ser His His Ala Arg Asp Gln Ile Leu Lys Arg 350 355 360	1589
acg gag gag tta aag tgaaaaagat gattgccgtt gcgttgactg ccgtcttcgc Thr Glu Glu Leu Lys 365	1644
aaggcattgtc gtttaagtt ttgcgtctca gccgaaggga gatgccgagt ttgccggcg agccattttt ctgcgtcata agccggctca gctgatggcg ggcagagcga tctttctcga cagctttgac ggaaattcgc cagccgcctg acaaaaacacc gcataaccct gcttgcacc ggacaagctc tcttcgaaaaa ggcgcgcag cggcgctttt tttatgaaag caaatataac cgccgtccct gcaaatcgct tgcgaagatt aaaaatatga aacacatgac aggaatggcg ctcacccgct tttggtcgaa tcctattgaa aaatctgccc gatttatagt gcttgcatt ctataaatcc ttataatggc cttAACGCCA atgtgaggca tgccaataga cagattgcag ggaaattct atactgaaca gcgcattta gcatgtatc	1704 1764 1824 1884 1944 2004 2064 2104

<210> 149

<211> 368

<212> PRT

<213> *Bacillus licheniformis*

<400> 149

Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala Gly Met Leu Asn Gln 1 5 10 15
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Trp Tyr Val Met Ile Lys Arg His Glu Val Ser Gln Ala Val Ser Ile 20 25 30

Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met Glu Glu Asn Gln Asp 35 40 45

Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg His Lys Leu Leu Thr 50 55 60

Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu Asp Ile Gln Glu Gln 65 70 75 80
--

Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile Glu Tyr Tyr Tyr Phe 85 90 95

Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys Asp Tyr Thr Asn Ala 100 105 110
--

Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu Arg Thr Ile Pro Asp 115 120 125
--

10295.204.ST25.txt

Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu Ala Ile Ala Tyr Tyr
130 135 140

Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His Ala Lys Thr Ala Leu
145 150 155 160

Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln Lys Ala Ile Ser Asn
165 170 175

Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu Phe Arg Phe Asp Glu
180 185 190

Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp Ala Ala Leu Ile Lys
195 200 205

His His Val Leu Leu Gly Met Ala His His Asn Leu Gly Leu Ser Tyr
210 215 220

Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His His Phe Lys Glu Ala
225 230 235 240

Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr Gly Ile His Ser Met
245 250 255

Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn Val Val Lys Glu Ala
260 265 270

Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala Glu Lys Ala Gly Glu
275 280 285

Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His Ala Leu Tyr Asp Glu
290 295 300

Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu Tyr Leu Lys Thr Ile
305 310 315 320

Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe Asp Ile Ala Leu Tyr
325 330 335

Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala Glu Tyr Phe Glu Glu
340 345 350

Ser His His Ala Arg Asp Gln Ile Leu Lys Arg Thr Glu Glu Leu Lys
355 360 365

<210> 150

<211> 1381

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

10295.204.ST25.txt

<222> (501)..(881)

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caggaggctt aaaagaagaa gtagagaagg aaattaatca aatggaagaa gatcaggact		180	
tactccttta ctatcagttg atgtgtttt gacatcaatt aatgttagaa tattnagaac		240	
ctactaacaa aagaaaacaa ggacaatcaa taaacaaatt gttggcccaa atcgaggagc		300	
ctcgaagaga tttaaatggc ctccttagtt actactcatt ttcccttagg ggcatgtatg		360	
aatttgagaa aaaacagtac atcaaagcaa tagagttt tcgaaacgca gaaaaacagt		420	
tggctctcat tacgatgtta tagaacaagc cgagttcac tttaaatgg ctgaagcata		480	
ctacatcatg aaacagacac atg tat cat ata tta agg gcc ttt aaa ata tac		533	
Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr			
1 5 10			
aat aat cat gaa ctc tac aca gtc cgt aaa atc caa tgt tta ttt gtt		581	
Asn Asn His Glu Leu Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val			
15 20 25			
atc gcg ggt aac tat gac gat tta atg cgc cat gac aaa gcc tta ccc		629	
Ile Ala Gly Asn Tyr Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro			
30 35 40			
cac ctg gaa aat gca ctt gaa tta gcg ata gag atc gac aat aaa agg		677	
His Leu Glu Asn Ala Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg			
45 50 55			
ctc att agt tct gcc tat ttt aat ata gcc gac tgt cat gaa tgt atg		725	
Leu Ile Ser Ser Ala Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met			
60 65 70 75			
gga gac att gat gca gca gtt gaa tat gct gaa aaa gcc gta gag att		773	
Gly Asp Ile Asp Ala Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile			
80 85 90			
aat cta aaa gaa gaa tat aac aac cta cca caa tca tta tat tac tct		821	
Asn Leu Lys Glu Glu Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser			
95 100 105			
act caa ctt ctt ttt aag cag aaa aac tac gag cgc gca atc gag ata		869	
Thr Gln Leu Leu Phe Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile			
110 115 120			
ttt ctt att ggt tagacaaaca gctcgaaat tcaacgatac cctattcact		921	
Phe Leu Ile Gly			
125			
tctctatgg aatatcttga ggcgttat atctattctg tgaataaaga agagatTTA		981	
gaggtatTTA aatacttggg ggagaataaa atatttgcatacatagaaga gctttcgctt		1041	
gaagtctcta accaatacct tgaaagaaaa gaccatagaa actcaatcga gttccttcaa		1101	
aaaatgatgt atgggcaaac aaaaattaaa aaaggggagt gtctctatga gtatTTaaaa		1161	
gctcgTTatt cccatTTtag ccGCCGCGTT attAACGATG ggtattAGCG ttGTTTCAGC		1221	
aACCGACCAG TCTGACGGCG TATATCAAAT CGCTACCCGT AAGCAAACGT AAGAAACGCC		1281	
CCAAAATGTGG GGCCTTTT ATTCTACGG TTCTTAACG TAAACATCG TGATTAACCT		1341	

10295.204.ST25.txt

cttatacgct gtcggtaaga ttaacgtata ccattccgac

1381

<210> 151
<211> 127
<212> PRT
<213> *Bacillus licheniformis*

<400> 151

Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr Asn Asn His Glu Leu
1 5 10 15

Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val Ile Ala Gly Asn Tyr
20 25 30

Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro His Leu Glu Asn Ala
35 40 45

Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg Leu Ile Ser Ser Ala
50 55 60

Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met Gly Asp Ile Asp Ala
65 70 75 80

Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile Asn Leu Lys Glu Glu
85 90 95

Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser Thr Gln Leu Leu Phe
100 105 110

Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile Phe Leu Ile Gly
115 120 125

<210> 152
<211> 1735
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1235)

<400> 152	ggcttggccc	cgacggaggc	ggacacttct	tttagagcg	gagaatcggt	gaaaactgcgg	60
	ccaaagaatt	gatttggagc	ggaaaaaat	tgacgggggc	cgaagcgcac	gagcttcgga	120
	tgcagacgc	cgtattcagc	ggggactccg	gccgtttgc	gcatctat	cttggaaagc	180
	ttctgcacgc	tccgctggca	gcgatgattg	agacaaaaaa	gatctatcag	gcgttgaatg	240
	gaggcaggct	gcagaaaacg	cttgaactcg	agaaaacggc	ccagatgaaa	atgaggctga	300
	caagcgacca	ttaggaaggg	atccgcgcac	tttagaaaa	gccccagccg	caatttaacc	360
	gtcagcaagt	ataacaagag	cggtccggca	ggaaattgac	cttggaaat	gatgtgcaga	420

10295.204.ST25.txt

aacaattgta aaaaaattta agtttccata aaatgattca taagatacag atctgtacga	480
agtcttggga ggcggcgaaa ttg aaa cag aag att cca tct gaa tac gtt gct Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala	533
1 5 10	
aga aag ctg aat gat tgg tac aac gcc att cgg aaa aat cag atc gcc Arg Lys Leu Asn Asp Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala	581
15 20 25	
gcc agt gaa tca ttg aaa gcg gaa att tta aat gat ttt caa gac atg Ala Ser Glu Ser Leu Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met	629
30 35 40	
gaa gaa aat cgg gac gtc ctg ctc tac tat tcg ctg ctt gaa ttc agg Glu Glu Asn Arg Asp Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg	677
45 50 55	
cat aaa ctg atg ctc agc tat ttg aaa ccg aaa gag act gaa aat att His Lys Leu Met Leu Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile	725
60 65 70 75	
gaa aaa aac ctc cgc gac tta gaa gaa aaa gaa gac caa atg acg ggt Glu Lys Asn Leu Arg Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly	773
80 85 90	
tta tta aac tat tat tac tgg ttt ttt aaa ggg atg tat gag ttc aaa Leu Leu Asn Tyr Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys	821
95 100 105	
caa aag cgg ttc gtc aaa gca atc ggc tgc tat aaa acg gct gaa caa Gln Lys Arg Phe Val Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln	869
110 115 120	
aaa gtc agc gca ctg gaa gac gag gtt gaa aaa gcg gaa ttt tat tat Lys Val Ser Ala Leu Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr	917
125 130 135	
aag ctt gcg gaa atc tac tat tat atc aac cag aga tac ctg tcg atc Lys Leu Ala Glu Ile Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile	965
140 145 150 155	
aac tat gcg acg cta gct tcc gac att ttt aac cgg tat gaa acg cta Asn Tyr Ala Thr Leu Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu	1013
160 165 170	
aaa gaa aaa aag att ttc tgc gat ttt atc att gcc ggt aat tgg gtt Lys Glu Lys Lys Ile Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val	1061
175 180 185	
gaa tcg atg aca tac gga ccc gcg ctg aaa agc ctg gcc aat gcg ctt Glu Ser Met Thr Tyr Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu	1109
190 195 200	
gaa gac gcc agg aaa atc aaa aac agc cat ttg acg gca gcc gct cat Glu Asp Ala Arg Lys Ile Lys Asn Ser His Leu Thr Ala Ala Ala His	1157
205 210 215	
ttt aat ttg gga aat tgc tat ttc cac caa gaa tcg tac cgg gaa gcc Phe Asn Leu Gly Asn Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala	1205
220 225 230 235	
tca gat cat atg gag cgc cct ttc cat ttt tgaacaggaa agttcatcat Ser Asp His Met Glu Arg Pro Phe His Phe	1255
240 245	
atattcccaa agtgctgtac aacttgatgt acgtccgtct caagcagggg aaccatgccg	1315

10295.204.ST25.txt

gagctgccgc ctgttatgaa	aaaggcatcc gaagcgcggc atcgctcggg gatgaagaac	1375
acgcggcaaa gcttaacatt	ctgtgcgggc tgtatTTAGA cggagggat cagaaagccg	1435
tggaaaacgg atttgattat	ttggagtcaa atcatttata tgctgctgtt gaagagctgg	1495
cttagatgc agcccagtat	tataatcaaa ttgagcggct gaaagattcc atttttact	1555
atgaaaagtg cgctcaggca	agtcgaaaaa tcaaaagggg agatgcgtt tatgaaagct	1615
aaactgttgt tcgtcgcgg	tcgtcgcgtt gtcgctggct gttgtttaa cgtcttcaag cttttggca	1675
gatgcgggga aagccccttc	cttgtatgcg gacaaaatga tcacgactga caaggagct	1735

<210> 153

<211> 245

<212> PRT

<213> *Bacillus licheniformis*

<400> 153

Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala Arg Lys Leu Asn Asp	
1	5 10 15

Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala Ala Ser Glu Ser Leu	
20	25 30

Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met Glu Glu Asn Arg Asp	
35	40 45

Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg His Lys Leu Met Leu	
50	55 60

Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile Glu Lys Asn Leu Arg	
65	70 75 80

Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly Leu Leu Asn Tyr Tyr	
85	90 95

Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys Gln Lys Arg Phe Val	
100	105 110

Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln Lys Val Ser Ala Leu	
115	120 125

Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr Lys Leu Ala Glu Ile	
130	135 140

Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile Asn Tyr Ala Thr Leu	
145	150 155 160

Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu Lys Glu Lys Lys Ile	
165	170 175

Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val Glu Ser Met Thr Tyr	
180	185 190

10295.204.ST25.txt

Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu Glu Asp Ala Arg Lys
 195 200 205

Ile Lys Asn Ser His Leu Thr Ala Ala Ala His Phe Asn Leu Gly Asn
 210 215 220

Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala Ser Asp His Met Glu
 225 230 235 240

Arg Pro Phe His Phe
 245

<210> 154
 <211> 2116
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1616)

<400> 154	attcctcgta aaaggcgccg atcgctcg cgcctttcc cttaaagca tcataatgt	60
	atgtgatgcc ctcaacagcc ttttgactt tggcgatttc gtctgattgt tgttttaatt	120
	gttccagcgt ttgatctatt gcatttgca gcccgtgaac atcaagagtc ttcatggcat	180
	tctcctctaa tcctttcat tacaatcagt atatagttt ccactttata gaaagtactt	240
	ggtaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatatttat	300
	tgattcattt cgattaccgt aaacaagttt gtttagcat tcttaggct ctgtgactaa	360
	accaaaaagc catttgttt aaatttgtct ttcggatca cggaaatttc gtttttggg	420
	ctgatagaag ttttgcattt atgaattgtt tttttttttt taacataaaa aggatgttag	480
	ctggaaaggaa atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile	533
	1 5 10	
	aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa	581
	Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu	
	15 20 25	
	gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa	629
	Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu	
	30 35 40	
	gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat	677
	Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His	
	45 50 55	
	gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa	725
	Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys	
	60 65 70 75	
	tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc	773
	Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly	
	80 85 90	

10295.204.ST25.txt

ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser. 95 100 105	821
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys 110 115 120	869
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr 125 130 135	917
aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met 140 145 150 155	965
tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr 160 165 170	1013
gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile 175 180 185	1061
gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys 190 195 200	1109
gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu 205 210 215	1157
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala 220 225 230 235	1205
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala 240 245 250	1253
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg 255 260 265	1301
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu 270 275 280	1349
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val 285 290 295	1397
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu 300 305 310 315	1445
aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu 320 325 330	1493
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn 335 340 345	1541
gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile 350 355 360	1589

10295.204.ST25.txt

aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga	1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile	
365 370	
cccttgcttt gggcttggc gtcgtgtcga gcgcattccat tcacacatct gttgaacaac	1696
aacatgcaga attttctgtta gcatctaggc tcgcaacata attgtgtttg ggcaggtcat	1756
gtgatggcct gccttttgg tgaaagaatt atttttagttt gaaaaccaga acgattgtgt	1816
taatactcat cttcttcgt cccttgtgtt ggaatttca tcatatcaat atttgaatat	1876
gcggctgtcc gcattattaa caattttaaa tttttgcac aaattttata caaaggcaga	1936
caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc	1996
aaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctcttttgt	2056
ttattcctca tcaaagcggagagccgccaataaacgcactgaccaact gttgtccgca	2116

<210> 155

<211> 372

<212> PRT

<213> *Bacillus licheniformis*

<400> 155

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp	
1 5 10 15	

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys	
20 25 30	

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu	
35 40 45	

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu	
50 55 60	

Tyr Leu Phe Pro Ala Glu Lys Leu Ser Lys Ser Asp Tyr Leu Arg	
65 70 75 80	

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr	
85 90 95	

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile	
100 105 110	

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val	
115 120 125	

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val	
130 135 140	

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu	
145 150 155 160	

10295.204.ST25.txt

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
355 360 365

Leu Tyr Glu Ile
370

<210> 156
<211> 1576
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1268)

<400> 156

10295.204.ST25.txt

cgaggccctcc attccaaaac gagtactggg acctgcata agacgggatc tatgtcgata	60
tcgtttcagg gaagccgctg tttcatcgc ttgacaaatt tgacgcacac tgccgctggc	120
caagcttcac aaaaccggtc gatgccggag aaatcgaga aaagctggac acttcacacg	180
gcatgattcg gactgaggtg agaagcaagt ctgccgattc ccacatggc cacgtgttc	240
cgacccggacc cgacccggac ggccctgcgc attgcataa ttccagccgc ctccggtttg	300
tgccgaagga cgacccgtgaa aagaaggat acggcataa tgtcaaactg tttgaacgca	360
agaaatccgg agagggaaagc tgaggagagc agcatgcaag atgatcctt tttcaaagg	420
tcatctttt ttagaggatt ttctgctctg aaagcgaaaa aacattacaa tagatcatct	480
tgagaaaaga ggcagccgtt gtg aca tcc att tca aac aca gaa gac cgt tat	533
Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr	
1 5 10	
tta atg ctg aca tgc agc aaa aaa att gaa tcc cat tat cat ata tac	581
Leu Met Leu Thr Cys Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr	
15 20 25	
aca gat gag gag atc ccg cag atg ttt tcc tct cat ttt ctg cag ctg	629
Thr Asp Glu Glu Ile Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu	
30 35 40	
cag gac gat ttt ccg ctg aca gag ctg tac tcc ctg ctc gtt cgg aca	677
Gln Asp Asp Phe Pro Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr	
45 50 55	
ccc gaa att tta aaa cga aat tat gtt cat gtg aaa agc tct tat aag	725
Pro Glu Ile Leu Lys Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys	
60 65 70 75	
cg gat ctg cct ttt acg atg aaa aag tcg ctc ttt gat ctt ggc tat	773
Arg Asp Leu Pro Phe Thr Met Lys Ser Leu Phe Asp Leu Gly Tyr	
80 85 90	
att ctt gat gaa gaa ttg ttt tat tcc atc agg ctt gca gat tgg aaa	821
Ile Leu Asp Glu Glu Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys	
95 100 105	
gga gat tcc cct ggt gta cgg gca gag tgg ggg acg gag aaa tcg ctc	869
Gly Asp Ser Pro Gly Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu	
110 115 120	
att gac ggc tgc cgc atg atg cag gct tat gat aca ttg tct atc aat	917
Ile Asp Gly Cys Arg Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn	
125 130 135	
gaa gcg ttt gcg aag gaa aag ctg ctg cgc aag tat cct ttt tat gag	965
Glu Ala Phe Ala Lys Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu	
140 145 150 155	
gaa ggc atc att cag ctg tgc tac tcg gaa gaa ggc gaa ccg	1013
Glu Gly Ile Ile Gln Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro	
160 165 170	
att gga tgt gct gag ctt tat ctc gat cac gac gaa aac gtt gct aaa	1061
Ile Gly Cys Ala Glu Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys	
175 180 185	
atc gaa gaa gtc gcc att ttg gag cca tac cag cgg aaa ggc tat gga	1109
Ile Glu Glu Val Ala Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly	
190 195 200	

10295.204.ST25.txt

tcg ggc ctt atc aag cag atg ctc acc gcc gcc aaa caa tcg ggc atg Ser Gly Leu Ile Lys Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met 205 210 215	1157
gaa tcg tgc tat ctt gta act tcg gga agc gat cag gtg aaa acg ttt Glu Ser Cys Tyr Leu Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe 220 225 230 235	1205
tat gaa aag ctg ggc ttt cag cag aag gaa aag ctc acg aca ata ttt Tyr Glu Lys Leu Gly Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe 240 245 250	1253
aaa tat ttg ttc gta taaagttaggc aggtgcacat accaattggg acttggcctg Lys Tyr Leu Phe Val 255	1308
cataggctgg ggtgttagact ttatacgaaa ggatgataag cctgtgcatt actcccatTA ttgctgtcct actggaggat acggctacgg gttcacgga agaacacatt tgactcatcg ttgtcctctt tattttgctc atcattgtcg gtgcggcttt catttgctag ctaaaagccc gacgccccggc gcttgacatg ctcacaaagc cttcctccgg aaggTTTTT ttggTTTTG ttggaaaATT ttgcattcgt atgtaata	1368 1428 1488 1548 1576

<210> 157
<211> 256
<212> PRT
<213> *Bacillus licheniformis*

<400> 157

val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr Leu Met Leu Thr Cys
1 5 10 15

Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr Thr Asp Glu Glu Ile
20 25 30

Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu Gln Asp Asp Phe Pro
35 40 45

Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr Pro Glu Ile Leu Lys
50 55 60

Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys Arg Asp Leu Pro Phe
65 70 75 80

Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr Ile Leu Asp Glu Glu
85 90 95

Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys Gly Asp Ser Pro Gly
100 105 110

Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu Ile Asp Gly Cys Arg
115 120 125

Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn Glu Ala Phe Ala Lys
130 135 140

10295.204.ST25.txt

Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu Glu Gly Ile Ile Gln
 145 150 155 160

Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro Ile Gly Cys Ala Glu
 165 170 175

Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys Ile Glu Glu Val Ala
 180 185 190

Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly Ser Gly Leu Ile Lys
 195 200 205

Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met Glu Ser Cys Tyr Leu
 210 215 220

Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe Tyr Glu Lys Leu Gly
 225 230 235 240

Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe Lys Tyr Leu Phe Val
 245 250 255

<210> 158

<211> 1783

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1283)

<400> 158

cctgc当地aa agccgttaaa caagcaaaaa cgcctgaccc gtttagggagg cggttatattt

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120

ttattgacaa acgcaaacga ttttttcgt cccggcccgc agtaagactg gcagccgatt

180

tccactttt catccggatc aatttcttc agacggggca aaagcgtctt taaattggtg

240

gcctggcaat cgtcgatac tcgaaattca tttagccattt catacgcttc ctttcgtttt

300

gttcatctgt ctttatgaaa ggcattcaac tgtgccgaac tttataaaa aatgacacca

360

tccttcattt tacaaggatt ctttcattcc tgcaaggatc ggcgtaaaaa aatcagttcc

420

tattctttt gcaaacttgt ataaatattt tccaaaatgg acaatctaacc accaatactg

480

acaatggag ttgagaagtg atg aaa caa aga caa gac gct tgg tct gag gaa

533

Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu

1

10

aat gat tta ctg ctt gct gaa acg gta ttg cgg cat gtc agg gaa ggg

581

Asn Asp Leu Leu Ala Glu Thr Val Leu Arg His Val Arg Glu Gly

15

20

25

agc aca cag ctg aac gcc ttc gag gaa gtc gga gac aga ctg aac agg

629

Ser Thr Gln Leu Asn Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg

30

35

40

10295.204.ST25.txt

aca tca gcc gcc tgc ggt ttt aga tgg aac gca gtt gtc cgc cac caa Thr Ser Ala Ala Cys Gly Phe Arg Trp Asn Ala Val Val Arg His Gln 45 50 55	677
tac gaa aaa gca ttg cag ctg gct aaa aaa cag agg aag caa aga atg Tyr Glu Lys Ala Leu Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met 60 65 70 75	725
cgc gcc ctc gga aac gga cag ccg gcg aaa aaa cgc tta tta tac aag Arg Ala Leu Gly Asn Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys 80 85 90	773
ccg ccg gtc gaa acg aat gct gaa cct cct gca gaa agc gtt gtt gag Pro Pro Val Glu Thr Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu 95 100 105	821
cag aag aaa gca acc gca gat tca agc gaa cag cag ccg atc gcc agc Gln Lys Ala Thr Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser 110 115 120	869
gag cat ctg cct tat gtt gat gag agc ttt aaa gaa gag tta gct agt Glu His Leu Pro Tyr Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser 125 130 135	917
tta tct cac ctt cta tcg cca aat cag ccg cag gcc ggc cat aca gcc Leu Ser His Leu Leu Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala 140 145 150 155	965
gat aca tcg aaa gac atg acg atc gat gat gtg atc cgc ttc ctg caa Asp Thr Ser Lys Asp Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln 160 165 170	1013
aac tat aca gga aac gaa gaa caa act gcc gct tta aaa atg gaa aat Asn Tyr Thr Gly Asn Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn 175 180 185	1061
gaa cgt tta aaa cag gaa aac gaa gaa ctg acg aag aaa gtt gaa aag Glu Arg Leu Lys Gln Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys 190 195 200	1109
ctt gaa gcg gaa gtc aaa aag ctg gaa aaa gac cag aca acc atc cag Leu Glu Ala Glu Val Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln 205 210 215	1157
gaa gac tac gaa acg ctc gta aaa att atg aac cgt gca aga aaa cta Glu Asp Tyr Glu Thr Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu 220 225 230 235	1205
gtt tta ttc gaa gaa gac gaa cac gct gcg ccc gcc ttc aaa atg gac Val Leu Phe Glu Glu Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp 240 245 250	1253
cgg aac ggc aat tta gaa aaa atg gct gaa tagcgctctc agaggatgcg Arg Asn Gly Asn Leu Glu Lys Met Ala Glu 255 260	1303
gcagagacgt tcagggcagca aggactgaca atgcatacaa acatTTTCG atacgaggat	1363
accccTTTCT ttaaaaaagg gggtatTTT acCTTCTGC ggCTTGTtT tatATGACAA	1423
aaatttcata atAGGGATAG caattcataa ggCGGGGTAT tcGATGAAGT ttGTTTATA	1483
tgcggTTCAG ttCGGCACTG CGGCCCTTT GTTTTGTT TCTGCATTGG CAAGCTGGTA	1543
tcaaggcagc gagCTTTAA AGGTGCCGTG GGAGTGGAAA TATACAGCCA AGTTACAAG	1603
ttggCTGTAC GGAGAGGACT CCATAAAAA CGCACATAAT ATTCACAGC TTGATTTT	1663

10295.204.ST25.txt

cgtctatgcg gccaaagcata cgccggcaac cgttattttt atggccgtca gtttggcgta 1723
tatcatcgct ttggcggtt atcttctcat caaaaacatat gtaaaaacgaa aaagcgcttc 1783

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<212> PRT
<213> *Bacillus licheniformis*

<400> 159

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Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg Thr Ser Ala Ala Cys
35 40 45

Gly Phe Arg Trp Asn Ala Val Val Arg His Gln Tyr Glu Lys Ala Leu
50 55 60

Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met Arg Ala Leu Gly Asn
65 70 75 80

Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys Pro Pro Val Glu Thr
85 90 95

Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu Gln Lys Lys Ala Thr
100 105 110

Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser Glu His Leu Pro Tyr
115 120 125

Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser Leu Ser His Leu Leu
130 135 140

Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala Asp Thr Ser Lys Asp
145 150 155 160

Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln Asn Tyr Thr Gly Asn
165 170 175

Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn Glu Arg Leu Lys Gln
180 185 190

Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys Leu Glu Ala Glu Val
195 200 205

Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln Glu Asp Tyr Glu Thr
210 215 220

10295.204.ST25.txt

Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu Val Leu Phe Glu Glu
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Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp Arg Asn Gly Asn Leu
245 250 255

Glu Lys Met Ala Glu
260

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gtgcagacgt	gttcgggatg	tagtccaatt	tttcgatgac	ttccaaaacc	cgcttccccc	300										
tttcttcaga	tacataggg	tgatcggtca	gtactcttga	aacagttgtt	tttgacacat	360										
tacttaattt	tgcaatttcg	tcaatcgtag	gcataaaagtc	acttcctgaa	aaaaagagtt	420										
gttatggtat	cgattccatc	attnaagata	tgtcatgaaa	tatgacaattt	tccccaaaata	480										
ataaaaaatgg	ggtgaaatgg	atg	aaa	acc	gca	aac	aatg	act	tgc	acg	533					
		Met	Lys	Thr	Ala	Asn	Glu	Asn	Met	Thr	Cys					
		1					5			10						
agc	aaa	cag	cta	ttt	gtc	ctt	ctg	aat	gat	ttg	aag	gaa	gga	aag	ctc	581
Ser	Lys	Gln	Leu	Phe	Val	Leu	Leu	Asn	Asp	Leu	Lys	Glu	Gly	Lys	Leu	
		15					20				25					
gct	ggt	gaa	tgc	cgt	ata	gac	gac	aca	ctg	gcc	aat	caa	aaa	tta	aaa	629
Ala	Gly	Glu	Cys	Arg	Ile	Asp	Asp	Thr	Leu	Ala	Asn	Gln	Lys	Leu	Lys	
		30				35					40					
gag	aca	ttg	cag	cag	gat	caa	ttc	gac	ata	acc	gcc	aat	ttg	ctg	aac	677
Glu	Thr	Leu	Gln	Gln	Asp	Gln	Phe	Asp	Ile	Thr	Ala	Asn	Leu	Leu	Asn	
		45			50					55						
aga	atg	gat	tcc	ccg	ccc	tcc	aga	gtt	gac	ttt	atg	ccg	ctt	cat	cga	725
Arg	Met	Asp	Ser	Pro	Pro	Ser	Arg	Val	Asp	Phe	Met	Pro	Leu	His	Arg	
		60			65				70					75		
ctg	atc	aca	gaa	gaa	gta	gat	gac	gtg	gtt	cat	gcg	gtg	aaa	gac	773	
Leu	Ile	Thr	Glu	Glu	Glu	Val	Asp	Asp	Val	Val	His	Ala	Val	Lys	Asp	
		80					85						90			
gtg	ctg	ccg	acc	ggg	caa	ttt	aca	agc	ggt	ttt	tat	gtt	ggc	gta	ttt	823
Val	Leu	Pro	Thr	Gly	Gln	Phe	Thr	Ser	Gly	Phe	Tyr	Val	Gly	Val	Phe	
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10295.204.ST25.txt

gaa gct gaa ata gct gct ttt ttg agc aaa aag cat gtc atg gct tca Glu Ala Glu Ile Ala Ala Phe Leu Ser Lys Lys His Val Met Ala Ser 110 115 120	869
tcc agc gga acc gat gcc atg att gtc gcg ctg aag gct gcg ggt gtt Ser Ser Gly Thr Asp Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val 125 130 135	917
gga caa ggt gat gaa gtc att atg cct gca aac agc ttt gct gca acg Gly Gln Gly Asp Glu Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr 140 145 150 155	965
gaa aac gcc gtc ctc gca gct gga ggc act ccg att ttc tgc gat att Glu Asn Ala Val Leu Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile 160 165 170	1013
gac cct gtt aca ttt tgc atg gat cct tca gaa att gaa gca tgt gtc Asp Pro Val Thr Phe Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val 175 180 185	1061
act ttg aaa acg aaa tgc att ttg cct gta cac ctt tat gga aag ctg Thr Leu Lys Thr Lys Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu 190 195 200	1109
cct gac atg gaa gcc att gca aaa acc gct gat aaa tac ggc atc ccg Pro Asp Met Glu Ala Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro 205 210 215	1157
att att gaa gac gcc tgc cag gcg atc ggc gtt tcc gat ctg gga aaa Ile Ile Glu Asp Ala Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys 220 225 230 235	1205
aac agc ctt tgc tcc ata tta agc ttc aat ccg tat aaa aat ctc ggc Asn Ser Leu Cys Ser Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly 240 245 250	1253
act tgc gga aaa gcc ggc gca att gtg acg gat gat cca tca ttt gca Thr Cys Gly Lys Ala Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala 255 260 265	1301
tcc gca tgc atg gaa tat atg tat cac ggc ttt gaa ctg aat caa aaa Ser Ala Cys Met Glu Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys 270 275 280	1349
aat aaa aag gcg gct gac tac ggc ttt aac gct aag att gat aat ctg Asn Lys Ala Ala Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu 285 290 295	1397
caa gcc gct att gga ctg gca agg atg aaa tat ctt tct tta aat aat Gln Ala Ala Ile Gly Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn 300 305 310 315	1445
ctg aag cgc tta tat tta gca gat cgt tat att gcg cat ttg cag cag Leu Lys Arg Leu Tyr Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln 320 325 330	1493
tat gaa gac aga ggt ctg atc aaa ttg cct caa atg acc gat gat cat Tyr Glu Asp Arg Gly Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His 335 340 345	1541
gta tgg cat ttg ttt aca att aaa ata cta aac gga aat cgt gac caa Val Trp His Leu Phe Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln 350 355 360	1589
gtc aaa gat atg atg ctt aaa ttt cat aat gtc caa aca gat ata tac Val Lys Asp Met Met Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr 365 370 375	1637

10295.204.ST25.txt

tac ccg att tta tcc cat cat caa aac aca cca ctt gta aaa gcc aat	380	385	390	395	1685
Tyr Pro Ile Leu Ser His His Gln Asn Thr Pro Leu Val Lys Ala. Asn					
ttt cgg cac aca tca ctg ccg gtc act gaa tca gtg cat aaa caa atg	400	405			1733
Tyr Arg His Thr Ser Leu Pro Val Thr Glu Ser Val His Lys Gln Met					
ctt cag ctt cct ctc tat ccg ggg ctc acc gta gaa gaa caa gac aaa	415	420			1781
Leu Gln Leu Pro Leu Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys					
gtt atg gag gcc tta att gat gtc gta tca tgaaacactt tctttcaca	430	435			1831
Val Met Glu Ala Leu Ile Asp Val Val Ser					
ccttgcagca agtaaacaag ccgaagtacg ccgtatttg cgattttgat gagacatatt					1891
tcgcccacag catcaccgat gaatcgagaa aagcgctcat ggacccttgaa acatttattc					1951
attcgcacca tcttgcac aagattttgc tcggctgggt gaccgggagc agcctgtcat					2011
ccgttcttgc aaaaatgaag cggggaggct ttcgatatct tccgcattt gtcgccgtg					2071
accttggcac tgaaatcact tatttctctg aagaaggcca agtctctgat aaagattggg					2131
aagcccgatt gcaagaatca aatttctccc atgatctggt cgaagaaatc aagcagactc					2191
tctctaaaaa atatgagatt gcgcttgtc ctcagactca gcatggcttt tccccgtata					2251
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<210> 161

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<213> *Bacillus licheniformis*

<400> 161

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Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu Ala Gly Glu Cys Arg
 20 25 30

Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys Glu Thr Leu Gln Gln
 35 40 45

Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn Arg Met Asp Ser Pro
 50 55 60

Pro Ser Arg Val Asp Phe Met Pro Leu His Arg Leu Ile Thr Glu Glu
 65 70 75 80

Glu Val Asp Asp Val Val His Ala Val Lys Asp Val Leu Pro Thr Gly
 85 90 95

Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe Glu Ala Glu Ile Ala
 100 105 110

10295.204.ST25.txt

Ala Phe Leu Ser Lys Lys His Val Met Ala Ser Ser Ser Gly Thr Asp
115 120 125

Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val Gly Gln Gly Asp Glu
130 135 140

Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr Glu Asn Ala Val Leu
145 150 155 160

Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile Asp Pro Val Thr Phe
165 170 175

Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val Thr Leu Lys Thr Lys
180 185 190

Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu Pro Asp Met Glu Ala
195 200 205

Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro Ile Ile Glu Asp Ala
210 215 220

Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys Asn Ser Leu Cys Ser
225 230 235 240

Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly Thr Cys Gly Lys Ala
245 250 255

Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala Ser Ala Cys Met Glu
260 265 270

Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys Asn Lys Lys Ala Ala
275 280 285

Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu Gln Ala Ala Ile Gly
290 295 300

Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn Leu Lys Arg Leu Tyr
305 310 315 320

Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln Tyr Glu Asp Arg Gly
325 330 335

Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His Val Trp His Leu Phe
340 345 350

Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln Val Lys Asp Met Met
355 360 365

Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr Tyr Pro Ile Leu Ser
370 375 380

10295.204.ST25.txt

His His Gln Asn Thr Pro Leu Val Lys Ala Asn Tyr Arg His Thr Ser
 385 390 395 400

Leu Pro Val Thr Glu Ser Val His Lys Gln Met Leu Gln Leu Pro Leu
 405 410 415

Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys Val Met Glu Ala Leu
 420 425 430

Ile Asp Val Val Ser
 435

<210> 162
 <211> 2143
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (501)..(1643)

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	gttttatttc atccctctgc ttttgtcagg gtttcggccc ggattcaaaa cggcgccgtt	180	
	gttatggcat cgagcgtcat ccaagcggat gcagacgtcg gcatccacgc gattgtcaac	240	
	acaggtgcga tcgtcgaaca cgacaatcgg atcggcgatt acgttcatct ttcgccccga	300	
	acgggtttaa ccggcggcgt gacagttatg gaaggcgctc atctcggcgc gggAACGGCG	360	
	gtcattcccg gaaagacagt cggacgctgg agcgtgacgg gagcgggggc agccgtgatt	420	
	cacgacattc ctgataattt caccgcagtc ggagtccctg caagaatgat caaataacag	480	
	cagtaaaaag ggtaaaaaac atg agt cag aat aag cga att tat tta tca ccg	533	
	Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro		
1	5	10	
ccg cac atg agc gga gac gag gag cgc tat gta gcc gaa gcg ttt cgg	581		
Pro His Met Ser Gly Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg			
15	20	25	
aca aac tgg atc gcg ccc ctc ggt ccc ctt gtc gac aca ttt gaa gaa	629		
Thr Asn Trp Ile Ala Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu			
30	35	40	
aag ctt gcc gcc tat gcg ggg acg tcc gga gcc gcg gca gtc agc tca	677		
Lys Leu Ala Ala Tyr Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser			
45	50	55	
gga aca gct gcg atc cac ctg gcc ttg aaa ttg ctc ggc gtc ggc aaa	725		
Gly Thr Ala Ala Ile His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys			
60	65	70	75
ggc gat acg gtc ttc tgc tct tct ttt acg ttt gta gcg agc gcc aat	773		
Gly Asp Thr Val Phe Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn			
80	85	90	
ccg atc ata tat gag cag gct gaa ccg gtt ttc att gat tct gaa ccg	821		

10295.204.ST25.txt

Pro Ile Ile Tyr Glu Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg	95 100 105	
gat aca tgg aac atg tcg ccc gag gcg ctt gaa cg ^g g ^c g ^c ctt gac gaa		869
Asp Thr Trp Asn Met Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu	110 115 120	
g ^c g ^a g ^c g ^g g ^c a ^g a ^a t ^t c ^t c ^c g ^a g ^c g ^t a ^t g ^t c ^t g ^t a ^a c ^t t ^t g ^a	125 130 135	917
Tyr Gly Gln Ser Ala Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg	140 145 150 155	965
t ^t t ^t g ^c g ^t g ^t c ^c t ^t g ^t a ^t t ^t g ^a g ^c a ^t g ^c g ^t c ^t g ^t g ^g t ^c t ^t g ^t	160 165 170	1013
Phe Ala Val Pro Val Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val		
t ^a t ^a g ^g c ^a a ^g a ^a a ^g c ^g a ^c t ^t c ^g g ^g a ^c t ^t t ^c g ^a a ^t t ^t t ^c g ^a	175 180 185	1061
Tyr Lys Gly Arg Lys Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser		
t ^t t ^c a ^a g ^g t ^t a ^a a ^a a ^t c ^t a ^c c ^c a ^c t ^c g ^g g ^g a ^t g ^t c ^t g ^t	190 195 200	1109
Phe Asn Gly Asn Lys Ile Ile Thr Thr Ser Gly Gly Met Leu Val		
a ^g c ^g g ^a t ^t g ^a a ^g c ^g g ^t a ^a a ^g g ^c c ^g t ^t t ^t t ^t g ^c a ^c t ^c c ^a g ^a	205 210 215	1157
Ser Asp Asp Glu Asp Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln		
g ^c g ^c g ^a c ^c g ^c a ^t t ^t c ^a t ^t c ^a g ^c c ^a g ^a a ^a g ^c g ^c t ^a c ^a a ^a	220 225 230 235	1205
Ala Arg Glu Pro Ala Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn		
t ^a c ^g g ^t a ^t g ^c a ^a t ^t g ^t g ^c g ^g a ^t c ^t g ^g c ^t a ^c t ^t g ^c	240 245 250	1253
Tyr Arg Met Ser Asn Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala		
g ^t t ^t c ^t g ^a t ^t g ^a c ^g g ^t a ^t g ^c a ^g c ^g g ^t t ^t t ^t g ^a c ^g c ^t t ^a	255 260 265	1301
Val Leu Asp Asp Arg Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr		
a ^a g ^a g ^c g ^c c ^t t ^c g ^t a ^t c ^g g ^a g ^t a ^t a ^a g ^t t ^t c ^c g ^a g ^c	270 275 280	1349
Lys Glu Ala Leu Ser Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala		
g ^g c ^t a ^t t ^c a ^a c ^g t ^g c ^t a ^c a ^c t ^t a ^c g ^t a ^c a ^c g ^a a ^a	285 290 295	1397
Gly Met Ser Asn Arg Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys		
a ^t t ^a a ^c a ^c a ^c c ^g g ^c g ^a c ^t a ^t c ^t g ^c a ^a t ^t g ^a a ^a a ^a	300 305 310 315	1445
Ile Gln Thr Thr Pro Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn		
a ^t t ^a g ^a g ^c c ^g c ^t t ^t t ^t g ^a a ^a c ^c t ^t t ^t c ^c c ^t t ^t t ^t	320 325 330	1493
Ile Glu Ala Arg Pro Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe		
a ^a g ^g g ^c g ^c g ^c t ^t t ^t c ^c g ^t a ^t g ^c g ^t t ^t t ^t g ^t c ^t t ^t	335 340 345	1541
Lys Gly Ala Ala Phe Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys		
g ^a t ^t t ^t c ^a g ^c g ^g c ^t t ^c g ^t c ^t g ^c t ^a g ^t a ^t g ^t a ^c g ^t	350 355 360	1589
Asp Leu Phe Gln Arg Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr		
c ^g a ^a g ^a c ^a g ^c g ^t a ^t c ^a a ^t c ^t g ^c g ^a c ^t c ^g a ^t a ^a		1637

10295.204.ST25.txt

Arg Lys Glu Gln Asp Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys
 365 370 375

tat aaa tgaggtgcta aacatggcga ttacatatcc catggacagc ttaaagcata 1693
 Tyr Lys
 380
 agctggcaga aattttggat gtcattccaa ggcattcatc agtcgttac ttggactacc 1753
 cgctatacgg aaacgtcggg gatctattga tcatgaaagg aacggaagct ttttttgaag 1813
 catacggcat caaggtgcgc gaaagatgga atgcggagaa tttcattccg ggccgcccga 1873
 ttccaaagga cgccatcatt gtttgcagg ggggcccga ttcggcgac ttgtaccctc 1933
 acttccagca gttcagagaa cgggtggtcg aacattaccc ggacaaccgg atcgtcatc 1993
 tgccgcagtc gatttattat gagcatgaag aaaatataat aaaaacgcgc ggcattttgg 2053
 cggctcaccc ggatctgcac ttattcacgc gggaaaaggc atcattcgat tttgccgtca 2113
 agcgtttcga agaggtgaaa aacatcaaaa 2143

<210> 163

<211> 381

<212> PRT

<213> *Bacillus licheniformis*

<400> 163

Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro Pro His Met Ser Gly
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Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg Thr Asn Trp Ile Ala
 20 25 30

Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu Lys Leu Ala Ala Tyr
 35 40 45

Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser Gly Thr Ala Ala Ile
 50 55 60

His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys Gly Asp Thr Val Phe
 65 70 75 80

Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn Pro Ile Ile Tyr Glu
 85 90 95

Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg Asp Thr Trp Asn Met
 100 105 110

Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu Ala Glu Arg Ala Arg
 115 120 125

Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu Tyr Gly Gln Ser Ala
 130 135 140

Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg Phe Ala Val Pro Val
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145

150

10295.204.ST25.txt

155

160

Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val Tyr Lys Gly Arg Lys
165 170 175

Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser Phe Asn Gly Asn Lys
180 185 190

Ile Ile Thr Thr Ser Gly Gly Met Leu Val Ser Asp Asp Glu Asp
195 200 205

Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln Ala Arg Glu Pro Ala
210 215 220

Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn Tyr Arg Met Ser Asn
225 230 235 240

Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala Val Leu Asp Asp Arg
245 250 255

Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr Lys Glu Ala Leu Ser
260 265 270

Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala Gly Met Ser Asn Arg
275 280 285

Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys Ile Gln Thr Thr Pro
290 295 300

Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn Ile Glu Ala Arg Pro
305 310 315 320

Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe Lys Gly Ala Ala Phe
325 330 335

Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys Asp Leu Phe Gln Arg
340 345 350

Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr Arg Lys Glu Gln Asp
355 360 365

Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys Tyr Lys
370 375 380

<210> 164

<211> 2107

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1607)

10295.204.ST25.txt

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gaattttcta	aaacgcctcg	tgccgaaaca	tgctcaagaa	tcggctataa	ctttcagcgg		120
aggcgggaat	acaaggccgc	tatctactgg	tatgagctgg	ccacaacatt	ggtgcctgat		180
tcaaataat	ggagcttcac	ctatccggca	tactatactt	ggtaccctca	tttgcaaatg		240
tgtgtgtct	attacaattt	aggagacttt	gaaaagtgcgt	atcatcataa	tgaagaggcg		300
aggaaatacc	gtcccgaaga	caaatccgtc	cttcataaca	aacagctgct	ggaagggaaa		360
ttaggcatta	acaatttagca	ttgtaaagac	ttactgaaca	atgttgtctt	tttttatga		420
ataaaatcaa	gccgtgccaa	tttagcggca	ggcatcataa	cttattttgg	aacttttgta		480
attttagagga	ggaacaaagg	atg atc ccg tta gtc	aat tta aaa cgt	caa ttt	Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe		533
		5	10				
caa aca gta	aaa cag gat	att tta aaa gag	ttt gaa cat	gtg ctg gac			581
Gln Thr Val	Lys Gln Asp	Ile Leu Lys	Glu Phe Glu His	Val Leu Asp			
15	20	25					
agc ggc caa	tat ata ttg	ggg cca aag gtt	gaa gaa tta	gag aaa aga			629
Ser Gly Gln	Tyr Ile Leu	Gly Pro Lys	Val Glu Glu Leu	Glu Lys Arg			
30	35	40					
ata gct gaa	aag ctt ggt	gta aaa gaa	gcg gtc	gcg gtc	gcc aac gga		677
Ile Ala Glu	Lys Leu Gly	Val Lys Glu Ala	Val Ala Val	Ala Val	Ala Asn Gly		
45	50	55					
acg gat gca	ttg gtg	ctg acg	ctt gaa	gct ttc	ggc atc	ggc aaa ggg	725
Thr Asp Ala	Leu Val	Leu Thr	Leu Glu Ala	Phe Gly Ile	Gly Lys Gly		
60	65	70	75				
gat gaa gtg	att acg acc	ccg ttc act	ttt ttc	gcc acc	gcc gaa	gcc	773
Asp Glu Val	Ile Thr	Pro Phe Thr	Phe Phe Ala	Thr Ala	Glu Ala		
80	85	90					
gtc tca agg	gtg ggg	gct gaa	cct gtc	ttt gct	gat gtc	gat cct gaa	821
Val Ser Arg	Val Gly	Ala Glu	Pro Val	Phe Ala	Asp Val	Asp Pro Glu	
95	100	105					
aca tac aat	ctt gat	ccg aaa	aaa ata	gaa gaa	aag atc	acc cct gct	869
Thr Tyr Asn	Leu Asp Pro	Lys	Ile Glu	Glu Lys	Ile Thr	Pro Ala	
110	115	120					
act aaa	gcg atc att	ccc gtc	cat atc	ttc gga	cag ccg	gct gat atg	917
Thr Lys Ala	Ile Ile Pro	Val His	Ile Phe	Gly Gln	Pro Ala	Asp Met	
125	130	135					
gac gag atc	atg gag	ctt gcc	aaa aaa cac	gga ctg	ctt gtg	att gag	965
Asp Glu Ile	Met Glu Leu	Ala Lys	His Gly	Leu Leu	Val Ile	Glu	
140	145	150	155				
gat gcc tgc	caa gcg	ttc ggc	gca tcg	tat aaa	gag cg	ccg cct gtc	1013
Asp Ala Cys	Gln Ala	Phe Gly	Ala Ser	Tyr Lys	Glu Arg	Pro Val Gly	
160	165	170					
agc atc ggg	gat gcc	gcc tgt	ttt tca	ttt ttc	cct aca	aaa aac ttg	1061
Ser Ile Gly	Asp Ala	Ala Cys	Phe Ser	Phe Phe	Pro Thr	Lys Asn Leu	
175	180	185					
gga aca ttg	gga gac	ggg gga	atg gtg	acg att	tca gac	ccg gat gca	1109
Gly Thr Leu	Gly Asp	Gly Gly	Met Val	Thr Ile	Ser Asp	Pro Asp Ala	

10295.204.ST25.txt

190	195	200															
gcc	caa	tta	aga	aca	ctc	aga	acc	cat	ggc	act	agc	aaa	aaa	ttc	1157		
Ala	Arg	Gln	Leu	Arg	Thr	Leu	Arg	Thr	His	Gly	Thr	Ser	Lys	Lys	Tyr		
205					210				215								
ttc	cat	gac	aaa	atc	gtt	ttc	aac	agc	cgt	ctt	gat	gaa	tta	cac	1205		
Phe	His	Asp	Lys	Ile	Gly	Phe	Asn	Ser	Arg	Leu	Asp	Glu	Leu	His	Ala		
220					225				230						235		
gca	gct	tta	ctc	att	ctt	ctt	gag	aaa	atc	gac	ggc	tgg	aat	gaa	caa	1253	
Ala	Ala	Leu	Leu	Ile	Leu	Leu	Glu	Lys	Ile	Asp	Gly	Trp	Asn	Glu	Gln		
					240				245						250		
aga	aga	aga	gtg	gcc	agc	cgc	tac	aga	gaa	gtt	ttg	aaa	acg	gcg	gag	1301	
Arg	Arg	Arg	Val	Ala	Ser	Arg	Tyr	Arg	Glu	Gly	Leu	Lys	Thr	Ala	Glu		
					255				260						265		
cac	ctc	aca	ctg	ccg	gca	gag	aaa	gag	gac	cgc	aca	cat	atc	tat	cat	1349	
His	Leu	Thr	Leu	Pro	Ala	Glu	Lys	Glu	Asp	Arg	Thr	His	Ile	Tyr	His		
					270				275						280		
ctc	tat	tgt	atc	ggc	gcg	aaa	aac	cgc	gac	tac	atc	ata	caa	tcg	ctg	1397	
Leu	Tyr	Cys	Ile	Gly	Ala	Lys	Asn	Arg	Asp	Tyr	Ile	Ile	Gln	Ser	Leu		
					285				290						295		
aaa	gag	cag	gac	att	cat	tca	ggt	gtg	tat	tat	cct	tgc	tgc	ctt	cat	1445	
Lys	Glu	Gln	Asp	Ile	His	Ser	Gly	Val	Tyr	Tyr	Pro	Cys	Cys	Leu	His		
					300				305						310	315	
ctg	caa	tcg	gtc	tat	tct	tca	ctg	cag	tac	aaa	aaa	ggc	gat	ttt	cct	1493	
Leu	Gln	Ser	Val	Tyr	Ser	Ser	Leu	Gln	Tyr	Lys	Lys	Gly	Asp	Phe	Pro		
					320				325						330		
ata	gcc	gag	tcc	ttg	tcc	gaa	acc	ctt	ttc	gcc	att	ccg	atg	gat	cct	1541	
Ile	Ala	Glu	Ser	Leu	Ser	Glu	Thr	Leu	Phe	Ala	Ile	Pro	Met	Asp	Pro		
					335				340						345		
ttt	cta	gcc	gcc	gag	gaa	caa	gat	cag	att	att	tct	gcg	ctg	ctg	aaa	1589	
Phe	Leu	Ala	Ala	Glu	Glu	Gln	Asp	Gln	Ile	Ile	Ser	Ala	Leu	Leu	Lys		
					350				355						360		
aaa	gga	gga	ggg	gaa	aag	tgacggttca	ttttggttta	atcggctgcg								1637	
Lys	Gly	Gly	Gly	Glu	Lys												
					365												
gctatatgtc	aagaaaacat	cttcaagcac	tggccgagtg	cgatgatgca	aagttgtcgg											1697	
ccgtcagtga	tttgcaggaa	gaaagaatga	aggaagcgga	agaatactat	gcttccctcg											1757	
ccgggtgagga	aagccgaatg	acccgctatc	cgcagtatca	agcgctgctt	tcagatccta											1817	
aaattgaagc	ggtcattatt	gcggcggtt	cgggactgca	cggcggaaatg	gccaaacatg											1877	
cgctgctggc	aggcaagcac	gtcatcgatcg	aaaaaccgat	gaccttgtca	ttacggatg											1937	
ccgatgagct	tatagaactg	gcggagcaga	acgggctgaa	gctcatggtc	tgccaccaga											1997	
tgccgccaccg	gccgatcatg	aaaaaaactga	aggaaacgat	tgaggaagga	aagctggaa											2057	
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<210> 165
<211> 369
<212> PRT
<213> Bacillus licheniformis

10295.204.ST25.txt

<400> 165

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Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
35 40 45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
50 55 60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
65 70 75 80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
85 90 95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
100 105 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
115 120 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
130 135 140

Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
145 150 155 160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
165 170 175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
180 185 190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
195 200 205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
210 215 220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
225 230 235 240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
245 250 255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
260 265 270

10295.204.ST25.txt

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
 275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
 290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
 305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
 325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
 340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
 355 360 365

Lys

<210> 166
<211> 2092
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1592)

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ggctattata agcatgacct gatcatcggt tcaaacagct ggatcgggca gcaatgttt	240
atacacggtg ccggcggggt tacaatcgga gaatttgcag gaatttgtcc gaacgtccgg	300
atacatgccg cttaccatac cgatcctgat aaacccgaca gtaccatttt gtttgcgg	360
cttacattcg ctcttattca tattgaagaa aactgcaaca tcgggatcg tgctgtatc	420
ctagcaggcg ttacgatagg cgcactcc aaaatcggag caaatgccgt cgtcaatcgc	480
aatattcccc cgtacagcat agcagttaggc gtgccggcaa aggtgattaa aaaccgaaaga	533
atgaaagatg aggatctctc atg atc aga ttg atc gag ccg tat att aca ttt	581
Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe	
1 5 10	
gaa gaa gtg caa gca gaa tta aag gag ata ttt tcc tct ggc atg ctg	
Glu Glu Val Gln Ala Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu	
15 20 25	
aca aaa ggc cct tat gtc aga aca ttt gct gat cat atg aga cag tat	629
Thr Lys Gly Pro Tyr Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr	
30 35 40	

10295.204.ST25.txt

gtc agt gca aag cat gct ttt tta aca aca tcg gca aca acg gct tta Val Ser Ala Lys His Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu 45 50 55	677
tcg atg tgc ctt aaa agc ctg aac gtg caa ccc gga gat gaa gta atc Ser Met Cys Leu Lys Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile 60 65 70 75	725
gtc tca gac ttc tcg ttc ccc gcc act gtc aat gta ata gaa gat tta Val Ser Asp Phe Ser Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu 80 85 90	773
gga gcc aag ccg gtt ttt gcc gat gtt gat ctt gaa aca ttt aac atg Gly Ala Lys Pro Val Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met 95 100 105	821
ctt cca gaa gaa ctg gaa agt caa atc acg tcc cgt aca aaa gcc gtt Leu Pro Glu Glu Leu Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val 110 115 120	869
ctt ttt gta gat gct ctt gga aac ccg aca ggc atc acc aac att aag Leu Phe Val Asp Ala Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys 125 130 135	917
caa att tgt aag gag tac ggc tta ccc ctt gtg gat gat gcc gct tgt Gln Ile Cys Lys Glu Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys 140 145 150 155	965
gcg atc ggc agc agc gaa tac ggc tgt aaa tcc gga aaa att gcc gat Ala Ile Gly Ser Ser Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp 160 165 170	1013
ctc acc tgt ttc agc ttt cac cca aga aag ctg ctt acg aca ggc gaa Leu Thr Cys Phe Ser Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu 175 180 185	1061
ggc ggg gca att aca acc gac cgg gaa gag ttg aaa gac tgg ctt tcg Gly Gly Ala Ile Thr Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser 190 195 200	1109
gtc aaa tta aac cat ggc gct gcc atc tct gac gga aaa ttg gat ttt Val Lys Leu Asn His Gly Ala Ala Ile Ser Asp Gln Lys Leu Asp Phe 205 210 215	1157
ata gat ttc ggc tac aac tac aga tta tcc gat atc caa gcc gct ctt Ile Asp Phe Gly Tyr Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu 220 225 230 235	1205
gga att aaa cag ctc caa aaa ctt gat gac atc att cat cgg aga aac Gly Ile Lys Gln Leu Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn 240 245 250	1253
ctt cag cag aaa gca tat agt gaa cag ctt gaa ccc ctc gga ttc caa Leu Gln Gln Lys Ala Tyr Ser Glu Gln Leu Glu Pro Leu Gln Phe Gln 255 260 265	1301
agt caa aaa atc ggt cca gcc gtt gta cac aac ata caa tcc gcc gtt Ser Gln Lys Ile Gly Pro Ala Val Val His Asn Ile Gln Ser Ala Val 270 275 280	1349
ttc aaa gtt cca aaa aac atc gtt cgc gac gaa ttg att caa tat ttg Phe Lys Val Pro Lys Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu 285 290 295	1397
agc gac tgc cat ata gag tcg act ttc ggc act tat tgt tta agc ggc Ser Asp Cys His Ile Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly 300 305 310 315	1445

10295.204.ST25.txt

act ccc tat tac cgc cg ^g aaa tac caa cag cta aaa tcg aat tct ctc Thr Pro Tyr Tyr Arg Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu 320 325 330	1493
ttt ctt gaa caa cat acg att acc ctc cct tgc cat gat gaa gtc gat Phe Leu Glu Gln His Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp 335 340 345	1541
tta gat cat gtg gtt tca gcc ata caa tca ttt atc aaa ttt aag gtt Leu Asp His Val Val Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val 350 355 360	1589
gat tagttcaaaa tatccgttc acagagaata gtgaacggg a tatttttat Asp	1642
tcttaataca agaataaaaa aacaggtagt aaaccataga tttaccacct gattcattca cataacaata cagcgaactt ccatgaaaaa aacattcac ctgttagatta agagacagtt ggaccgagaa tatatgcaaa tctgttagaa tgaaaatgct agtggatat tcgatgttt tacaaggatc gttaatatt tggacagaca atgtgtaact ctcaattgta caattagtt tcttaaaga gaaactgctc cgcaagaaaa acctacggaa cagcttccta atgagaatat taattagaaa gttttcgat ttggatatga ccgctgttc ctgttagcaag agttaacgct aatccagtga cgccaatctg aatagtagaa gggacagcag taacttaat catagcttct cccactaatg gagtacctac gctgattaaa	1702 1762 1822 1882 1942 2002 2062 2092

<210> 167

<211> 364

<212> PRT

<213> *Bacillus licheniformis*

<400> 167

Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe Glu Glu Val Gln Ala 1 5 10 15
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Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu Thr Lys Gly Pro Tyr 20 25 30

Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr Val Ser Ala Lys His 35 40 45

Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu Ser Met Cys Leu Lys 50 55 60

Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile Val Ser Asp Phe Ser 65 70 75 80
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Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu Gly Ala Lys Pro Val 85 90 95

Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met Leu Pro Glu Glu Leu 100 105 110
--

10295.204.ST25.txt

Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val Leu Phe Val Asp Ala
115 120 125

Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys Gln Ile Cys Lys Glu
130 135 140

Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys Ala Ile Gly Ser Ser
145 150 155 160

Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp Leu Thr Cys Phe Ser
165 170 175

Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu Gly Ala Ile Thr
180 185 190

Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser Val Lys Leu Asn His
195 200 205

Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe Ile Asp Phe Gly Tyr
210 215 220

Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu Gly Ile Lys Gln Leu
225 230 235 240

Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn Leu Gln Gln Lys Ala
245 250 255

Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln Ser Gln Lys Ile Gly
260 265 270

Pro Ala Val Val His Asn Ile Gln Ser Ala Val Phe Lys Val Pro Lys
275 280 285

Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu Ser Asp Cys His Ile
290 295 300

Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly Thr Pro Tyr Tyr Arg
305 310 315 320

Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu Phe Leu Glu Gln His
325 330 335

Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp Leu Asp His Val Val
340 345 350

Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val Asp
355 360

<210> 168
<211> 1663
<212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1163)

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	ggcatttttc cgtgcgccgt cactcttgcc tcgttggctg gaaaggcttt tacagaggaa	180
	atcacgagtc tcttcatttc gtccgcaagt ctgggaggag cgcttcttgc attcttgatc	240
	ggctggcga ttgatgcaag cgccagccgt gtcttcccgt ttttgctgtt cggcggattg	300
	gggggcttgc tgctggcgat cagcgcggtg attttttat ccggcctgca aaaaaacaag	360
	cagagtcat tggatatgta gatttattag gaagagatta caagcttagt aggattttt	420
	tcagcagccg tttaaaccgt tccatcttgc accataatat tgctagaaaa gggtgaagaa	480
	cgagaggaac ggtggggaaa atg aag aaa tca aac att gcc tgt atg tat att	533
	Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile	
	1 5 10	
	ttt ctt tta tta ata gga gcg ctt gca aat ctc acg acg gaa gag act	581
	Phe Leu Leu Leu Ile Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr	
	15 20 25	
	gcc caa tca tca ggc ggg cag cct gcc gtg att cct gat gaa gcg att	629
	Ala Gln Ser Ser Gly Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile	
	30 35 40	
	cgcg ctg cg att ttg gca aac agc gac agc ggg agc gac cag agc gtc	677
	Arg Leu Arg Ile Leu Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val	
	45 50 55	
	aaa cgc aaa atc agg gat gag gtc aat aaa caa att acg aaa tgg gtg	725
	Lys Arg Lys Ile Arg Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val	
	60 65 70 75	
	gaa aac ctg acc tcg gtt gag gaa gcg aga caa gtc atc agg tcg aag	773
	Glu Asn Leu Thr Ser Val Glu Ala Arg Gln Val Ile Arg Ser Lys	
	80 85 90	
	ctg cct gaa atc caa gag gtt gcc atg gat gtc atg aaa cgc gaa aat	821
	Leu Pro Glu Ile Gln Glu Val Ala Met Asp Val Met Lys Arg Glu Asn	
	95 100 105	
	gtt cgg caa tcc gtg tct gtc cgt ttt gat cgt gtt tca ttt ccg aca	869
	Val Arg Gln Ser Val Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr	
	110 115 120	
	aag cta tac ggc aat atg gtg tat ccg gcc gga gaa tat gag gct gtt	917
	Lys Leu Tyr Gly Asn Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val	
	125 130 135	
	tta att aca tta ggc aag gga gag gga gcc aac tgg tgg tgc gtc ctg	965
	Leu Ile Thr Leu Gly Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu	
	140 145 150 155	
	ttt ccg cca ctt tgc ttt ctt gat ttt tcc aat ggg gaa gcc gta aag	1013
	Phe Pro Pro Leu Cys Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys	
	160 165 170	

<210> 169
<211> 221
<212> PRT
<213> *Bacillus licheniformis*
<400> 169

Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile Phe Leu Leu Leu Ile
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20 25 30

Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile Arg Leu Arg Ile Leu
35 40 45

Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val Lys Arg Lys Ile Arg
50 55 60

Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val Glu Asn Leu Thr Ser
65 70 75 80

Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys Leu Pro Glu Ile Gln
85 90 95

Glu Val Ala Met Asp Val Met Lys Arg Glu Asn Val Arg Gln Ser Val
100 105 110

10295.204.ST25.txt

Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr Lys Leu Tyr Gly Asn
 115 120 125

Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val Leu Ile Thr Leu Gly
 130 135 140

Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu Phe Pro Pro Leu Cys
 145 150 155 160

Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys Ser Pro Glu Asp Glu
 165 170 175

Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu Lys Thr Asp Ala Ala
 180 185 190

Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys Glu Asp Lys Glu Val
 195 200 205

Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu Phe Ser
 210 215 220

<210> 170
<211> 1351
<212> DNA
<213> *Bacillus licheniformis*

<220>	170					
<221>	CDS					
<222>	(501)..(851)					
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cgttcagcca	atatgaaacg	catccgatgt	ataaacgtaa	cgaaatcatt	tccgatttga	120
aggtaataa	aggccgttag	caaaaaataa	accttgcac	atcagaaccg	atttcccttt	180
tgacgaaaaa	aggcgaaaat	atcgaatctg	ttaaaaaaga	aatcaaacag	aaagaagata	240
tccaggcccc	tgtcaaaaaaa	ggcacagagc	ttgggacgct	cgtttgaaa	aaggatggaa	300
aggtgctcgc	tgaaagtccct	tttgtcgctg	aaaaagatat	ggacaaagcg	ggatgtggaa	360
cgatgttcaa	gcccacgtat	acccactgga	cgaagtggag	tgaataatgc	cgaacggtca	420
ctagtttgt	cacggtgaag	gaatttataa	agtctgaagc	gaaacactca	ttatccgatt	480
taaaccagg	aggaatgagg	atg agc ctc gga atc gat att cac gtc	aaa gaa	Met Ser Leu Gly Ile Asp Ile His Val Lys Glu		533
		1	5	10		
tcc gta tta tgc att	cgg ttg aca ggt	gaa ctc gat	cac cat aca gca			581
Ser Val Leu Cys Ile	Arg Leu Thr Gly	Glu Leu Asp His His	Thr Ala			
15	20	25				
gaa acc ttg aga aaa caa gtc agt gac cat ctg	gaa caa acc gac att					629
Glu Thr Leu Arg Lys Gln Val Ser Asp His Leu Glu Gln	Thr Asp Ile					
30	35	40				
cgc cat att gtc atg aat ctt gca gac ctt tcg ttt	atg gac agt tca					677

10295.204.ST25.txt

Arg His Ile Val Met Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser			
45	50	55	
ggg ctt ggc gtc gtg ctc ggc aga tat aag gag att aag cag ctc ggc			725
Gly Leu Gly Val Val Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly			
60	65	70	75
gga gaa atg atc gtc tgc gcc att tcc cct gct gtc aaa cgt tta ttt			773
Gly Glu Met Ile Val Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe			
80	85	90	
gat atg tcc ggg ctg ttt aaa atc att cgc ctt gag caa tca gag cag			821
Asp Met Ser Gly Leu Phe Lys Ile Arg Leu Glu Gln Ser Glu Gln			
95	100	105	
cgt gca ctt gaa acg ttg ggg gtg gcg tca tgaaaaatga aatgaacatt			871
Arg Ala Leu Glu Thr Leu Gly Val Ala Ser			
110	115		
cagtttacag cgctcagcca aaatgaatcg tttcacggg tgacagtcgc tgctttatc			931
gctcagcttg acccgacgat gcatgaactg accgaaatta aaacggcgt atccgaagcg			991
gtcacaaaacg cgatcattca cggtatgaa aactcaggc agggaaacgt atatattcc			1051
gtcactctcg aggaccatat tgtctattt acgatccgc acgaaggagt cggcatccct			1111
aatcttgaag aagcgcgcca gcccctgttc acgacaaagc ctgaactcga gcggtcggga			1171
atgggcttta cgatcatgga aaatttcatg gatgatattt cgatcgactc ctcacctgag			1231
atgggaacca caatacactt aacaaagcac ttatcaaaaa gcaaagcgt ttgcaattaa			1291
gggagatttggatgt ggaggttaaa aaagaaaaacc agaacactca gcttaaagac			1351

<210> 171

<211> 117

<212> PRT

<213> Bacillus licheniformis

<400> 171

Met Ser Leu Gly Ile Asp Ile His Val Lys Glu Ser Val Leu Cys Ile			
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Arg Leu Thr Gly Glu Leu Asp His His Thr Ala Glu Thr Leu Arg Lys			
20	25	30	

Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile Arg His Ile Val Met			
35	40	45	

Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser Gly Leu Gly Val Val			
50	55	60	

Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly Gly Glu Met Ile Val			
65	70	75	80

Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe Asp Met Ser Gly Leu			
85	90	95	

Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln Arg Ala Leu Glu Thr	
Page 246	

100

10295.204.ST25.txt
105

110

Leu Gly Val Ala Ser
115

<210> 172
<211> 1438
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(938)

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	cgaacggtca ctatccattgt cacggtaag gaatttataaa agtctgaagc gaaacactca	120
	ttatccgatt taaaccaagg aggaatgagg atgagcctcg gaatcgatat tcacgtcaaa	180
	aatccgtat tatgcattcg gttgacaggt gaactcgatc accatacagc agaaaaccttg	240
	agaaaacaag tcagtgacca tctggAACAA accgacattc gccatattgt catgaatctt	300
	gcagacccTTT cgTTTATGGA cagttcaggg cttggcgtcg tgctcggcag atataaggag	360
	attaaggcagc tcggcggaga aatgatcgTC tgcccattt cccctgctgt caaacgttta	420
	tttgatatgt ccgggctgtt taaaatcatt cgccttgagc aatcagagca gcgtgcactt	480
	gaaacgttgg gggtggcgTC atg aaa aat gaa atg aac att cag ttt aca gcg	533
	Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala	
	1 5 10	
	ctc agc caa aat gaa tcg ttt gca cgg gtg aca gtc gct gct ttt atc	581
	Leu Ser Gln Asn Glu Ser Phe Ala Arg Val Thr Val Ala Ala Phe Ile	
	15 20 25	
	gct cag ctt gac ccg acg atg gat gaa ctg acc gaa att aaa acg gtc	629
	Ala Gln Leu Asp Pro Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val	
	30 35 40	
	gta tcc gaa gcg gtc aca aac gcg atc att cac ggt tat gaa aac tca	677
	Val Ser Glu Ala Val Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser	
	45 50 55	
	ggg cag gga aac gta tat att tcc gtc act ctc gag gac cat att gtc	725
	Gly Gln Gly Asn Val Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val	
	60 65 70 75	
	tat tta acg atc cgc gac gaa gga gtc ggc atc cct aat ctt gaa gaa	773
	Tyr Leu Thr Ile Arg Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu	
	80 85 90	
	gcg cgc cag ccc ctg ttc acg aca aag cct gaa ctc gag cgG tcg gga	821
	Ala Arg Gln Pro Leu Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly	
	95 100 105	
	atg ggc ttt acg atc atg gaa aat ttc atg gat gat att tcg atc gac	869
	Met Gly Phe Thr Ile Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp	
	110 115 120	
	tcc tca cct gag atg gga acc aca ata cac tta aca aag cac tta tca	917
	Ser Ser Pro Glu Met Gly Thr Thr Ile His Leu Thr Lys His Leu Ser	

10295.204.ST25.txt

125	130	135	
aaa agc aaa gcg ctt tgc aat taagggagat ttgttatgga tgtggagggtt Lys Ser Lys Ala Leu Cys Asn 140		145	968
 aaaaaaagaaaa accagaacac tcagcttaaa gaccatgaag tgaaagaact gattaaaaaac agccagaacg gcgatcaaaa agcaagggac ctcctcatag aaaaaaacat gcgtcttggtt tggctctgtcg ttcagcggtt tttgaacaga ggctatgagc ctgacgacct ctttcaaatac ggctgcatacg gcctcttgaa gtcgggtggac aaattcgatc tttcctatga cgttcgggtt tccacctacg ccgttccgat gattatcggc gagattcagc ggtttatcag agatgacgga accgtcaaag tgagccgctc gctgaaagaa ctcggcaaca aaatccggcg ggcgaaagac gagctttcca agtcaaacgg ccggattccg accgttcagg aaatcgccga ttatctcgaa atcagttcag aagaggtcgt gatggcccag gaagcggtcc gctctccctc			
			1028
			1088
			1148
			1208
			1268
			1328
			1388
			1438

<210> 173

<211> 146

<212> PRT

<213> *Bacillus licheniformis*

<400> 173

Met	Lys	Asn	Glu	Met	Asn	Ile	Gln	Phe	Thr	Ala	Leu	Ser	Gln	Asn	Glu
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Ser	Phe	Ala	Arg	Val	Thr	Val	Ala	Ala	Phe	Ile	Ala	Gln	Leu	Asp	Pro
				20			25					30			

Thr	Met	Asp	Glu	Leu	Thr	Glu	Ile	Lys	Thr	Val	Val	Ser	Glu	Ala	Val
				35		40						45			

Thr	Asn	Ala	Ile	Ile	His	Gly	Tyr	Glu	Asn	Ser	Gly	Gln	Gly	Asn	Val
				50		55					60				

Tyr	Ile	Ser	Val	Thr	Leu	Glu	Asp	His	Ile	Val	Tyr	Leu	Thr	Ile	Arg
				65		70			75			80			

Asp	Glu	Gly	Val	Gly	Ile	Pro	Asn	Leu	Glu	Glu	Ala	Arg	Gln	Pro	Leu
				85				90				95			

Phe	Thr	Thr	Lys	Pro	Glu	Leu	Glu	Arg	Ser	Gly	Met	Gly	Phe	Thr	Ile
				100			105				110				

Met	Glu	Asn	Phe	Met	Asp	Asp	Ile	Ser	Ile	Asp	Ser	Ser	Pro	Glu	Met
				115			120					125			

Gly	Thr	Thr	Ile	His	Leu	Thr	Lys	His	Leu	Ser	Lys	Ser	Lys	Ala	Leu
				130		135				140					

Cys	Asn
	145

10295.204.ST25.txt

<210> 174
<211> 5482
<212> DNA
<213> *Bacillus licheniformis*

<220>
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	ccatgaagag cctgacgc tt caagtcgatc cgaataattt cctttactgg attcagatcg	120
	gacgcggcgc caataaagaa gcgc ttgaga cggcccgtaa gctggaaaac aatgcacaga	180
	tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg	240
	atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattt aagcggacag	300
	cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg	360
	cggacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag	420
	aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt	480
	tgttggcagg aggcggagaa atg agt ctg tta tgg att ttt tat cat aaa aac	533
	Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn	
	1 5 10	
	tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc	581
	Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile	
	15 20 25	
	ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa	629
	Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu	
	30 35 40	
	aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac	677
	Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn	
	45 50 55	
	gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag	725
	Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys	
	60 65 70 75	
	gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa	773
	Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu	
	80 85 90	
	gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc	821
	Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile	
	95 100 105	
	gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg	869
	Val Ile Ser Ser Leu Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr	
	110 115 120	
	gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac	917
	Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp	
	125 130 135	
	ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga	965
	Gly Gln Trp Asn Val Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly	
	140 145 150 155	

10295.204.ST25.txt

gaa gaa gtg tcc gcc cct gtc tcc gtg caa aat gga gac gaa atc gca Glu Glu Val Ser Ala Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala 160 165 170	1013
ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile 175 180 185	1061
gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro 190 195 200	1109
agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg 205 210 215	1157
atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala 220 225 230 235	1205
cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro 240 245 250	1253
ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro 255 260 265	1301
ccg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu 270 275 280	1349
att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys 285 290 295	1397
aga gaa aaa aga gag cgg gtc tat acc ctt tac ctt gaa aac aaa Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys 300 305 310 315	1445
aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp 320 325 330	1493
ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile 335 340 345	1541
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln 350 355 360	1589
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu 365 370 375	1637
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln 380 385 390 395	1685
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile 400 405 410	1733
act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser 415 420 425	1781

10295.204.ST25.txt

gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe 430 435 440	1829
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu 445 450 455	1877
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro 460 465 470 475	1925
cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln 480 485 490	1973
ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu 495 500 505	2021
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca Asn Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr 510 515 520	2069
aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly 525 530 535	2117
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys 540 545 550 555	2165
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu 560 565 570	2213
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Ala Val Gln Ile Pro 575 580 585	2261
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc cgg Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg 590 595 600	2309
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro 605 610 615	2357
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp 620 625 630 635	2405
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu 640 645 650	2453
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn 655 660 665	2501
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr 670 675 680	2549
ggt tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597

10295.204.ST25.txt

gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys 700 705 710 715	2645
ggg ggc gga atg gcg cag ccg ttc cg aac att ccg cat ttg ctc gga Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly 720 725 730	2693
acg att act aac att gaa ggc agc aag aac ttc agc aac cg gcg ctt Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu 735 740 745	2741
gcg tcc att aag agc gag ctg aag aaa agg cag cg ctc ttt gat cag Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln 750 755 760	2789
tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys 765 770 775	2837
aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe 780 785 790 795	2885
gcc gag ctg aaa agc gaa gaa ccg gaa ttt atc cgc gag ctt gtc agt Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser 800 805 810	2933
gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr 815 820 825	2981
caa aaa ccg ggc atc atc gat gac cag att tgg agc aac tcc aga Gln Lys Pro Gly Gly Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg 830 835 840	3029
ttc aag gtc gcc ttg aag gtg cag gat gcg aat gac agt aaa gag atc Phe Lys Val Ala Leu Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile 845 850 855	3077
ctc aaa aac ggg gat gcg gct acc atc acg gta acg ggc cgc ggc tat Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr 860 865 870 875	3125
ttg caa gtc ggc aac aac gag gtg tat gaa ctg ttc cag tct gca tgg Leu Gln Val Gly Asn Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp 880 885 890	3173
agc gga gcc cct tac atg gag gac ggc tac ggc aca gag gat gaa gtg Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val 895 900 905	3221
gcg atc gtc aca gat acc gga tta att cct tta tca gat gtt gat gct Ala Ile Val Thr Asp Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala 910 915 920	3269
gat cgc gct gcg aaa aaa gag gct gtg acg gaa att tcg gca gtc gtc Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val 925 930 935	3317
gaa caa att gaa cgg att caa gcg gag atg gga atc gag aag ctc ccg Glu Gln Ile Glu Arg Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro 940 945 950 955	3365
agc cct tgg ctg ccg ccg ctt gaa gaa cgc ata ccg aaa acg cgc tat Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr 960 965 970	3413

10295.204.ST25.txt

ccg tcg gag gaa gcc gat gcc ttt aac ttt gcc tat atc gat gaa cct Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro 975 980 985	3461
gaa aag caa agc cag gag ccg atc agc tac cgc atg atg gaa gac ggc Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly 990 995 1000	3509
aat atc ggc atc gtc ggc tcg tca ggc tac gga aaa tcc ctg aca Asn Ile Gly Ile Val Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr 1005 1010 1015	3554
gcc acg acg ttc atg atg agc ttt gcc gaa cag tat acg ccg gaa Ala Thr Thr Phe Met Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu 1020 1025 1030	3599
gaa ttg cat tac tac att ttc gac ttt ggc aac gga acg ctg ctt Glu Leu His Tyr Tyr Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu 1035 1040 1045	3644
ccg ctt gca agg ctt ccg cac acc gcg gat tat ttc ctg atg gac Pro Leu Ala Arg Leu Pro His Thr Ala Asp Tyr Phe Leu Met Asp 1050 1055 1060	3689
caa acg aga aaa atc gag aaa ttt atg gtc cgg atc aag gcg gaa Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu 1065 1070 1075	3734
atc gag cac agg aaa aat ctc ttc cgt gca aaa gaa atc agc cat Ile Glu His Arg Lys Asn Leu 1085 Phe Arg Ala Lys Glu Ile Ser His 1080	3779
atc aag atg tac aat gcg ctg aat gag gaa aag ctg ccg ttt att Ile Lys Met Tyr Asn Ala Leu 1100 Asn Glu Glu Lys Leu Pro Phe Ile 1095	3824
ttc ata acg gtc gac aac ttt gac atc att aaa gac gaa atg cat Phe Ile Thr Val Asp Asn Phe 1115 Asp Ile Ile Lys Asp Glu Met His 1110	3869
gaa ctc gaa agc gaa ttt atc cag ttt tca cga gac ggc cag tcg Glu Leu Glu Ser Glu Phe Ile 1130 Gln Phe Ser Arg Asp Gly Gln Ser 1125	3914
ctt gga att tat tta atc ctg acc gcg aca agg gtc aat gca atc Leu Gly Ile Tyr Leu Ile Leu 1145 Thr Ala Thr Arg Val Asn Ala Ile 1140	3959
aga cag tcg ctc ttg aac aac ctg aaa acg agg gtt gtc cac tat Arg Gln Ser Leu Leu Asn Asn 1160 Leu Lys Thr Arg Val Val His Tyr 1155	4004
ctg atg gat cag tct gaa gca tat tcg att atc gga agg ccg gaa Leu Met Asp Gln Ser Glu Ala 1175 Tyr Ser Ile Ile Gly Arg Pro Glu 1170	4049
ttc agc ctt gaa ccg atc cct gga cgc gtt att atc aat aaa gaa Phe Ser Leu Glu Pro Ile Pro 1190 Gly Arg Val Ile Ile Asn Lys Glu 1185	4094
aac caa tac ttc gca caa atg ttt atg cct gtg gaa gcg gac aac Asn Gln Tyr Phe Ala Gln Met 1205 Phe Met Pro Val Glu Ala Asp Asn 1200	4139
gat atc gag ctg ttt gaa ggg atc aaa gcc gac att cag gcg atc Asp Ile Glu Leu Phe Glu Gly 1220 Ile Lys Ala Asp Ile Gln Ala Ile 1215	4184

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gca gaa	cgc tcg gaa ggc atg	aga aag ccg gcg cct	gtg ccg atg	4229
Ala Glu	Arg Ser Glu Gly Met	Arg Lys Pro Ala Pro	Val Pro Met	
1230	1235	1240		
ctg ccg	ctc gag ctt tcc gtc	aca cag ttt gtg aga	gat tat ccg	4274
Leu Pro	Leu Glu Leu Ser Val	Thr Gin Phe Val Arg	Asp Tyr Pro	
1245	1250	1255		
ctt cag	cct gaa aga ggc ctt	att cca atg gga ctc	gat gaa gaa	4319
Leu Gln	Pro Glu Arg Gly Leu	Ile Pro Met Gly Leu	Asp Glu Glu	
1260	1265	1270		
act gtc	gaa ccc gta tac ttt	aat ctt gag aaa aat	aag cac tgc	4364
Thr Val	Glu Pro Val Tyr Phe	Asn Leu Glu Lys Asn	Lys His Cys	
1275	1280	1285		
ctc att	atg ggt cag acg cag	cgc gga aaa aca aac	gtc atc aag	4409
Leu Ile	Met Gly Gln Thr Gln	Arg Gly Lys Thr Asn	Val Ile Lys	
1290	1295	1300		
atc atg	ctc gag cac ctg ctt	gac cat gac acg aaa	aaa atc gcc	4454
Ile Met	Leu Glu His Leu	Asp His Asp Thr Lys	Lys Ile Ala	
1305	1310	1315		
gtg ttt	gat tcg ata gac aga	ggg ctt tct caa tat	gcg aca gag	4499
Val Phe	Asp Ser Ile Asp Arg	Gly Leu Ser Gln Tyr	Ala Thr Glu	
1320	1325	1330		
gat caa	atc agc tat cta gaa	aca aaa gac gac att	ctg ctc tgg	4544
Asp Gln	Ile Ser Tyr Leu Glu	Thr Lys Asp Asp Ile	Leu Leu Trp	
1335	1340	1345		
ctc gct	gag acg gaa gaa att	tgc cgg aca agg gaa	gcg atg tat	4589
Leu Ala	Glu Thr Glu Glu Ile	Cys Arg Thr Arg Glu	Ala Met Tyr	
1350	1355	1360		
ttg gaa	gcc gtt aaa caa gga	gaa atc gcc aac ctt	gat ttc tca	4634
Leu Glu	Ala Val Lys Gln Gly	Glu Ile Ala Asn Leu	Asp Phe Ser	
1365	1370	1375		
ccg atg	gtc ttt att gtc gac	gga att tca cgg ttc	cag cag acg	4679
Pro Met	Val Phe Ile Val Asp	Gly Ile Ser Arg Phe	Gln Gln Thr	
1380	1385	1390		
atc gac	gca tcg att cag gac	aaa atg gcg atg ttc	atg aaa tct	4724
Ile Asp	Ala Ser Ile Gln Asp	Lys Met Ala Met Phe	Met Lys Ser	
1395	1400	1405		
tac gcc	cat tta ggt ttc cac	ttt ata cct gcc gga	aat cac agc	4769
Tyr Ala	His Leu Gly Phe His	Phe Ile Pro Ala Gly	Asn His Ser	
1410	1415	1420		
gag ttc	aca aaa ggc tat gat	tcg ctg aca agc gaa	gtc aag cag	4814
Glu Phe	Thr Lys Gly Tyr Asp	Ser Leu Thr Ser Glu	Val Lys Gln	
1425	1430	1435		
gtc aga	cac gcg atg cta ttg	atg aaa aaa tcc gag	cag aac ttg	4859
Val Arg	His Ala Met Leu Leu	Met Lys Lys Ser Glu	Gln Asn Leu	
1440	1445	1450		
att cag	ctc cca tat gaa cgc	cag gag ccg gaa att	ctg ccg ggc	4904
Ile Gln	Leu Pro Tyr Glu Arg	Gln Glu Pro Glu Ile	Leu Pro Glu	
1455	1460	1465		
ttt ggc	tat atc gtt gaa aac	ggc aaa gag agg aaa	att caa att	4949
Phe Gly	Tyr Ile Val Glu Asn	Gly Lys Glu Arg Lys	Ile Gln Ile	
1470	1475	1480		

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cct tta tgt gct gta gaa agg aag aaa gcg aaa tgacggaca	4992
Pro Leu Cys Ala Val Glu Arg Lys Lys Ala Lys	
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gtttttcat ttcatcggtg agaacccgac gaaaaaggta tcgaacgcga caagggaaat	5112
cgcgcgttgc aatgaggata ccggcggtt gaaagatgac ggaaccgtt atcaagatgc	5172
gctgctggaa aacgaaatct cggctccct ggtgaccgt ccggattata aatggacggt	5232
cgtcaaccgg agcgcagcag aaagcggact tgccggagaag caatacgatg cgattgtcta	5292
cattccgtcg gactttcgc aaaacattt aagctacaac catgagcgtc cgaaaaaagc	5352
ggagctggaa ttcaaaattc aggaccagct cgacgcccgtc aacaaggaaa aagtccagcg	5412
cgagcttcag gacgcgcaaa aaacggtgag caagaaaatg tcttcctgt actggcgctt	5472
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<211> 1494

<212> PRT

<213> *Bacillus licheniformis*

<400> 175

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Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile Gly Pro Asp Leu Lys	
20 25 30	

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr	
35 40 45	

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly	
50 55 60	

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser	
65 70 75 80	

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val	
85 90 95	

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu	
100 105 110	

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly	
115 120 125	

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val	
130 135 140	

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala	
Page 255	

145 150 10295.204.ST25.txt 155 160

Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
165 170 175

Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
180 185 190

Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
195 200 205

Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
210 215 220

Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
245 250 255

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
290 295 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
385 390 395 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
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420

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425

430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
435 440 445

Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
515 520 525

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
530 535 540

Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
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690

695

700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
785 790 795 800

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
805 810 815

Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
820 825 830

Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
835 840 845

Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
850 855 860

Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
865 870 875 880

Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
885 890 895

Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
900 905 910

Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
915 920 925

Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
930 935 940

Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
945 950 955 960

Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
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965

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970

975

Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
980 985 990

Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
995 1000 1005

Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
1010 1015 1020

Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu Glu Leu His Tyr Tyr
1025 1030 1035

Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
1040 1045 1050

Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile
1055 1060 1065

Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
1070 1075 1080

Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
1085 1090 1095

Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
1100 1105 1110

Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
1115 1120 1125

Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
1130 1135 1140

Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
1145 1150 1155

Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
1160 1165 1170

Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
1175 1180 1185

Ile Pro Gly Arg Val Ile Ile Asn Lys Glu Asn Gln Tyr Phe Ala
1190 1195 1200

Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
1205 1210 1215

Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu
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1220

1225

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1230

Gly Met Arg Lys Pro Ala Pro Val Pro Met Leu Pro Leu Glu Leu
1235 1240 1245

Ser Val Thr Gln Phe Val Arg Asp Tyr Pro Leu Gln Pro Glu Arg
1250 1255 1260

Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
1265 1270 1275

Tyr Phe Asn Leu Glu Lys Asn Lys His Cys Leu Ile Met Gly Gln
1280 1285 1290

Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
1295 1300 1305

Leu Leu Asp His Asp Thr Lys Lys Ile Ala Val Phe Asp Ser Ile
1310 1315 1320

Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu Asp Gln Ile Ser Tyr
1325 1330 1335

Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
1340 1345 1350

Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
1355 1360 1365

Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
1370 1375 1380

Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
1385 1390 1395

Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
1400 1405 1410

Phe His Phe Ile Pro Ala Gly Asn His Ser Glu Phe Thr Lys Gly
1415 1420 1425

Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met
1430 1435 1440

Leu Leu Met Lys Lys Ser Glu Gln Asn Leu Ile Gln Leu Pro Tyr
1445 1450 1455

Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly Phe Gly Tyr Ile Val
1460 1465 1470

Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile Pro Leu Cys Ala Val
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1475

1480

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1485

Glu Arg Lys Lys Ala Lys
 1490

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 <211> 3343
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	gaatataatc gaacaaaaca aggacgcaca ggaagggata atccaatgat tctgtatacg	180
	aaaatgcgc aggaaatcggttgcaggg caggcggaaa actcgaaatt aaaacagatc	240
	gatgtaaaca gcgtgccact tttagtcgag atgaacggag aggaagcaag ggacgttcag	300
	gttctcagca cgaacccgat ggattttta aaacaagaaa cggcccctgg gcagacgctt	360
	aaactgacat ttataaaata gctggagtgt ctcaaggata aatatgctat aatagggaa	420
	tccagaggaa aatcgcagcc gaaaaaaggc tgctttctct ttgttttac attttttaac	480
	acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa	533
	Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys	
1	5 10	
	caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga	581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly		
15	20 25	
tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta	629	
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val		
30	35 40	
gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg	677	
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp		
45	50 55	
ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt	725	
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe		
60	65 70 75	
tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt	773	
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu		
80	85 90	
tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt	821	
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe		
95	100 105	
cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa	869	
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln		
110	115 120	
aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg	917	
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser		

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125	130	135	
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Pro Asp Leu Gly Gly Met Ile Gly Ala	Leu Leu Phe Ala Ala	Ser	
140	145	150	155
tat ttt ctg ttt gca tct gca gga tct aaa	atc atc gcc gtc	ttc ctg	1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser	Lys Ile Ile Ala Val	Phe Leu	
160	165	170	
atc ttg atc ggc ctt ctt ttg att acg gat	cgg tcg ctt cag	gag acg	1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp	Arg Ser Leu Gln	Glu Thr	
175	180	185	
ctg atc aaa tgg atg acc ccg gtc gcc tcc	ttc atg aaa aac	cag tgg	1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser	Phe Met Lys Asn Gln	Trp	
190	195	200	
cag gcc ttt tta gca gat ctt aaa caa ttg	aaa aac agc tcg ccg	aaa	1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu	Lys Asn Ser Ser Pro	Lys	
205	210	215	
aag aaa tcc gga aaa aaa caa aag acg	cag aga aaa ccg	aaa gtg tct	1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln	Arg Lys Pro Lys Val	Ser	
220	225	230	235
gaa gag cct gta caa gaa gcg gac	ctt gat cca gat ccg	gtt att caa	1253
Glu Glu Pro Val Gln Glu Ala Asp Leu	Asp Pro Asp Pro Val	Ile Gln	
240	245	250	
tca gaa ccg att att tca agc ttt tcc	gac cgt gat gaa aag	ccc gaa	1301
Ser Glu Pro Ile Ile Ser Ser Phe Ser	Asp Arg Asp Glu Lys	Pro Pro Glu	
255	260	265	
gtt caa gct tac gaa gct ccg gcg	gct cct gct gaa cct	cct gct gag	1349
Val Gln Ala Tyr Glu Ala Pro Ala	Pro Ala Glu Pro Pro	Ala Glu	
270	275	280	
ccc gaa atc ggt gag gaa atg cag	gcc tcc ggc gcg	ccc gaa atc acg	1397
Pro Glu Ile Gly Glu Glu Met Gln Ala Ser	Gly Ala Pro Glu Ile Thr		
285	290	295	
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Phe Thr Glu Leu Glu Asn Lys Asp Tyr	Gln Leu Pro Ser Ile Gln Leu		
300	305	310	315
ctg gat gat ccg aag cac aca ggg	cag cag gcg gat	aaa aag aat att	1493
Leu Asp Asp Pro Lys His Thr Gly Gln	Gln Ala Asp Lys Lys	Asn Ile	
320	325	330	
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Tyr Asp Asn Ala Arg Lys Leu Glu Arg	Thr Phe Gln Ser Phe	Gly Val	
335	340	345	
aag gcg aaa gtc acc cag gtt cat ctc	ggc ccg gcc gtc	acg aaa tat	1589
Lys Ala Lys Val Thr Gln Val His Leu	Gly Pro Ala Val Thr	Lys Tyr	
350	355	360	
gaa gtc tat cct gat gtc ggc gtc	aaa gtc agc aaa	att gtc aac tta	1637
Glu Val Tyr Pro Asp Val Gly Val Lys	Val Ser Lys Ile Val Asn Leu		
365	370	375	
agt gac gac ttg gct tta gcg ctc	gcc ggc aag gat	atc cgc atc gaa	1685
Ser Asp Asp Leu Ala Leu Ala Ala	Lys Asp Ile Arg Ile Glu		
380	385	390	395
gcc ccg atc ccc gga aaa tcg gcg	att gga atc gaa	gtg ccg aat gcg	1733
Ala Pro Ile Pro Gly Lys Ser Ala Ile	Gly Ile Glu Val Pro Asn Ala		

400	405	410	
gaa gtg gcg atg gtt tcc ttg aaa gaa	gtg ctt gaa tcg aaa ctg aat		1781
Glu Val Ala Met Val Ser Leu Lys	Glu Val Leu Glu Ser Lys Leu Asn		
415	420	425	
gac cgg ccg gat gca aag ctg atg atc	ggc ctc ggc cg aac att tcc		1829
Asp Arg Pro Asp Ala Lys Leu Met Ile	Gly Leu Gly Arg Asn Ile Ser		
430	435	440	
gga gaa gcg gta ttg gca gag ctg aac	aaa atg ccc cac ctt ctt gtt		1877
Gly Glu Ala Val Leu Ala Glu Leu Asn	Lys Met Pro His Leu Leu Val		
445	450	455	
gca gga gcg acc gga agc ggg aaa	agc gtc tgt gtc aac ggg atc att		1925
Ala Gly Ala Thr Gly Ser Gly Lys Ser	Val Cys Val Asn Gly Ile Ile		
460	465	470	475
aca agc att ttg atg agg gca aag ccc	cac gaa gtg aag atg atg atg		1973
Thr Ser Ile Leu Met Arg Ala Lys Pro	Glu Val Lys Met Met Met		
480	485	490	
att gat ccg aaa atg gtc gag ctc aat	gtc tac aac ggg att ccg cat		2021
Ile Asp Pro Lys Met Val Glu Leu Asn	Val Tyr Asn Gly Ile Pro His		
495	500	505	
ttg ctc gct ccc gtc gtg aca gac ccg	aaa aaa gca tcg cag gct ttg		2069
Leu Leu Ala Pro Val Val Thr Asp Pro	Lys Lys Ala Ser Gln Ala Leu		
510	515	520	
aag aaa gtc gtc aac gaa atg gag cgg	cgc tac gaa ttg ttt tct cac		2117
Lys Lys Val Val Asn Glu Met Glu Arg	Arg Tyr Glu Leu Phe Ser His		
525	530	535	
acg gga acg aga aat atc gaa ggg tat	aac gac tat att aaa cgg atg		2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr	Asn Asp Tyr Ile Lys Arg Met		
540	545	550	555
aat gcc gca gaa gaa gca aag cag ccg	gag ctt cca tac atc att gtg		2213
Asn Ala Ala Glu Glu Ala Lys Gln Pro	Glu Leu Pro Tyr Ile Ile Val		
560	565	570	
att gtg gac gag ctt gcc gac ctg atg	atg gtc gct tcc tct gat gtt		2261
Ile Val Asp Glu Leu Ala Asp Leu	Met Met Val Ala Ser Ser Asp Val		
575	580	585	
gaa gac tcg atc aca agg ctt tcg caa	atg gcc agg gcg ggc atc		2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln	Met Ala Arg Ala Ala Gly Ile		
590	595	600	
cac ctg atc att gcg acg cag agg cct	tcg gtc gat gtt atc aca ggg		2357
His Leu Ile Ile Ala Thr Gln Arg Pro	Ser Val Asp Val Ile Thr Gly		
605	610	615	
gtc att aaa gcc aac att ccg tca agg	atc gct ttc agc gta tcg tct		2405
Val Ile Lys Ala Asn Ile Pro Ser Arg	Ile Ala Phe Ser Val Ser Ser		
620	625	630	635
cag acc gac tcc agg acg att ctt gat	atg gga ggc gct gaa aaa ctt		2453
Gln Thr Asp Ser Arg Thr Ile Leu Asp	Met Gly Gly Ala Glu Lys Leu		
640	645	650	
ctc ggc aga ggg gac atg ctg ttt ctc	cct gtc ggc gcc aat aaa ccg		2501
Leu Gly Arg Gly Asp Met Leu Phe	Leu Pro Val Gly Ala Asn Lys Pro		
655	660	665	
ctc cgc gtt caa ggt gcc ttt ctg tca	gac gaa gaa gtt gaa aaa gtt		2549
Leu Arg Val Gln Gly Ala Phe Leu Ser	Asp Glu Glu Val Glu Lys Val		

10295.204.ST25.txt
670 675 680

gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg		2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met		
685 690 695		
att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt		2645
Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu		
700 705 710 715		
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta		2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val		
720 725 730		
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cg		2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg		
735 740 745		
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga		2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly		
750 755 760		
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc		2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu		
765 770 775		
tct tct tgagaagaga gttcttgaaa aacataattt cattatgtaa actaaaaaac		2893
Ser Ser		
780		
atctatttat ttatggaca aaacatgata tagttatcct caattaaaga taatggaaat		2953
ctgatctgtc agacggaggaa aaaacatgtc gataaaagct gacatcaacg gttatgttt		3013
aagggtattt atcggataaa agatgatatt caaatgggg tctttgcga aatgaacgg		3073
ctcccgagtg aatttgagct gtcaaagatg cttgggtgtga gcagaacggc tttgcgttag		3133
gcccgttagaa tactgaaaga agaaaacgtc atcatcagaa ggcattggagt cggacatttt		3193
gtaaatgcca gaccgttatt tctatcggt attgagcagc tgaacagcgt cacaatgt		3253
atcgagcagg caagcatgac gccggaaacc attttatgt cctcacaggt taccgctccc		3313
actgaagaag atatgctccg gtttcaatat		3343

<210> 177

<211> 781

<212> PRT

<213> *Bacillus licheniformis*

<400> 177

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys	
1 5 10 15	

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala	
20 25 30	

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe	
35 40 45	

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu	
50 55 60	

10295.204.ST25.txt

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
180 185 190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

10295.204.ST25.txt

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
450 455 460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
580 585 590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
595 600 605

10295.204.ST25.txt

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625 630 635 640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780

<210> 178
<211> 1735
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1235)

<400> 178
gatattgtgc gtaaacacta tcttccgatc cggtaagac gagttcgacg tcgggattct 60
gttttgcaaa ctgctcaaac cgttgtttaa ttgcagtctg gcctttctct ttgtacgctt 120
tttgatcaat ccattcgctg aaatacgcaa tggaagtctc cttgctgccg atatcttgct 180
gaataatgtc gttcagttca tcgatattgt ctttcgact tctcaaaatc tcatcctcga 240
gcgtgctgct ggccgtaaaa tatgaagtaa ccgaaagaac caagatcgga attgttaaaa 300
tgaatataaa tgagaaaatt aatttttag aaatagaagg acgtttcgtc caatttaaaa 360

10295.204.ST25.txt

gcttttcat gtgtgattcc ccttctcta cttttatcg agacgggtc tatttttaa	420
ataaaaaaaag cgaaaatta gaccgttgc ctgcccaga atcaggcata cgctaataaa	480
aaaggaaaag ggtgtatcct atg ata agt gtt tcg ggc tac cgg ctc cgt cct Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro	533
1 5 10	
gag gat atc gaa aaa ctg aat gtc agt cag acg cag aga gac atc gca Glu Asp Ile Glu Lys Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala 15 20 25	581
aac cgg atg ctg gcc atg ccg tcc gga tat aga tac ggt tca atc tca Asn Arg Met Leu Ala Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser 30 35 40	629
gaa ctg tta ttt gag ctg aga ttc aga gag cat acc gtc aaa tcg gcc Glu Leu Leu Phe Glu Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala 45 50 55	677
aga gag ctg atc aac agc gga gcg aag ttt gcc acc ttt tca aag aca Arg Glu Leu Ile Asn Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr 60 65 70 75	725
tac ggg aat gaa gag ttt tgg agg gtg acg cct gag ggg gct ttg gag Tyr Gly Asn Glu Glu Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu 80 85 90	773
ttg aag tac agg gca ccg gct tca aag gcg att cga aat att ttt gaa Leu Lys Tyr Arg Ala Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu 95 100 105	821
agc ggc cct tct tat gct ttt gag tgc gcg act gcg att gtc atc att Ser Gly Pro Ser Tyr Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile 110 115 120	869
ttt tat atg gcg ctt ctc aaa acg atc ggc gac cag aca ttt gac cgg Phe Tyr Met Ala Leu Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg 125 130 135	917
aat tat caa agg atc att tta tac gat tgg cac tat gag cgg ctg ccg Asn Tyr Gln Arg Ile Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro 140 145 150 155	965
atc tat acg gat aaa gga aac gac tac ctt ccg gga gac tgc ctg tat Ile Tyr Thr Asp Lys Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr 160 165 170	1013
ttc aag aac cct gaa ttc gat ccc tca aga ccg cag tgg cgc gga gaa Phe Lys Asn Pro Glu Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu 175 180 185	1061
aat gct att tta ctt gaa aat aat ctc tat gcg gca cac ggc ctg ggg Asn Ala Ile Leu Leu Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly 190 195 200	1109
atc tta agc ggc gaa aca atc att gaa aaa ctg aac ggg ctg aga aag Ile Leu Ser Gly Glu Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys 205 210 215	1157
cct cat gca cag acg tcc gcc tat ctg ctt tcc caa gtg acg ccg gtt Pro His Ala Gln Thr Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val 220 225 230 235	1205
gat att ccg gca tta att caa atg atc aga tagcacatcg gccggcacaa Asp Ile Pro Ala Leu Ile Gln Met Ile Arg 240 245	1255

10295.204.ST25.txt

gctgatccat cagtccttc accgtcgaaa gtcgacggt ggccgcacg ctctgtccgg	1315
ccccacaatga catgttatcc gtattccgt caagcttcgc ctgtttctc atcggttgcg	1375
tcagcggtt ttgcagagga taaggcagcg cttcagcttc ttcctggcgt ctgtcttcca	1435
tccactgatt gacgatgcct cttgccggct tccccgagaa caaacgggtc aggcttggt	1495
cggtttcaac cgcttcgaac aattttgtt tgtaggcagg gtgtgttccg ctttcttcgc	1555
acgtcaaaaa agcggtaccg atttgaacgc cctgtgcgcc gagggcaaaa gctgcagcaa	1615
cacctctttt gtcaaaaaatg ccgcccgtg cgataactgg aaccgacaca tgatctgccg	1675
cttggggaat taaagccatc gagccgacag caggctctcc cttcgaaaaatg aagaaggctc	1735

<210> 179

<211> 245

<212> PRT

<213> Bacillus licheniformis

<400> 179

Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro Glu Asp Ile Glu Lys			
1	5	10	15

Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala Asn Arg Met Leu Ala		
20	25	30

Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser Glu Leu Leu Phe Glu		
35	40	45

Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala Arg Glu Leu Ile Asn		
50	55	60

Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr Tyr Gly Asn Glu Glu			
65	70	75	80

Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu Leu Lys Tyr Arg Ala		
85	90	95

Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu Ser Gly Pro Ser Tyr		
100	105	110

Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Phe Tyr Met Ala Leu		
115	120	125

Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg Asn Tyr Gln Arg Ile		
130	135	140

Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro Ile Tyr Thr Asp Lys			
145	150	155	160

Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr Phe Lys Asn Pro Glu		
165	170	175

10295.204.ST25.txt

Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu Asn Ala Ile Leu Leu
 180 185 190

Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly Ile Leu Ser Gly Glu
 195 200 205

Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys Pro His Ala Gln Thr
 210 215 220

Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val Asp Ile Pro Ala Leu
 225 230 235 240

Ile Gln Met Ile Arg
 245

<210> 180
 <211> 1405
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(905)

<400> 180	aggctatact acagtctgag gtgattgaaa ttggccaaac gaaaagcaaa tcatgtataa	60	
	aatggaaatga acaatgcgaa acgccaagga aacggcgccg gatatattga aaatgatcag	120	
	cacatactca ctgaggcgga acgccaaaac aacaaaaaac ggaaaaccaa tcaataaata	180	
	cgaaagatcc ttcatgaata tcttaggagg taaaacatt gacaaataaa aacgacggca	240	
	aagatatgca caaaaacgca ccgaaaggag ctcagccggg gcagccagag ctttgagcg	300	
	gaagcaaaaa agtaaaaaac cgaaaccata caagacaaaa acacaattcc agtcacgata	360	
	tgtAACATT TTTCCGCGCC TTTCACGGCG CGGTTTTT CCTTACCGCG CGTCACCCCTG	420	
	aggcgttgc caccctcatt cacatgaatt caaagggtgtg cataatctaa tggtaaggct	480	
	aggtatggag gaatgctcca atg aca aat aca aaa cgt ttc gat tcc gca gat	533	
	Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp		
1	5	10	
ttt gat aaa gaa tgg atg aaa cag ttt gtt gac gac cct ttt ctc ctc	581		
Phe Asp Lys Glu Trp Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu			
15	20	25	
tat gat gaa act tta ccg att gac ctt tat gaa acg agc act gaa tat	629		
Tyr Asp Glu Thr Leu Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr			
30	35	40	
ata att gaa gca gat tta agc cac ttg aat gtc cgg cat ctt gac ttg	677		
Ile Ile Glu Ala Asp Leu Ser His Leu Asn Val Arg His Leu Asp Leu			
45	50	55	
acg ttt tca ggc tac gat ttc aag ctt gca gtt aaa acc gat gag cag	725		
Thr Phe Ser Gly Tyr Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln			
60	65	70	75

10295.204.ST25.txt

ctt tac gag aaa tcg ctg atg ctt cct ttc ttt ttg aat gac aaa cag Leu Tyr Glu Lys Ser Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln 80 85 90	773
atc gaa gcg gaa tgc gaa aac aac att ctt gca gtt aaa atc aat aaa Ile Glu Ala Glu Cys Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys 95 100 105	821
gaa tca agc aaa gat gac att tcg ctt tca atc aat att cct ttt ata Glu Ser Ser Lys Asp Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile 110 115 120	869
tca aac ctg cac aac aag cag aac ccg gac agc gct taaaacactt Ser Asn Leu His Asn Lys Gln Asn Pro Asp Ser Ala 125 130 135	915
gccccatccggg tttttttccg ttcgttcgtc aaatatcctc tagcaattct ctagggccga ttagggaatc gctatacaat agattatgtt ctagcatctc ttttgaccag gccgggtgtcc cattttatat tattttttct atgttcttct aaaacgcctt catgtaaaat aggttataga caaaggagtg atgagagatg ctggaaggat gtttttatg gctgatgctc gcttggatcg tcatcatgat cgccctcttg tcaatccggcg gtttttcat gtttcgcaaa tttttaaaaaa ggctgcctaa agaagatggg aaatctgagc tggactggca ggattattat attgaacaga caaggcattt gtggaatgac gaagaaaaag aactgcttga ggaattgggtt tcacccgtac ccgagctgtt tcgcgatgta gcaaaagcaa aaatcgccgg taagatcggg gagcttgcatt tgaaagaaaa 1405	975 1035 1095 1155 1215 1275 1335 1395

<210> 181

<211> 135

<212> PRT

<213> Bacillus licheniformis

<400> 181

Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp Phe Asp Lys Glu Trp 1 5 10 15
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Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu Tyr Asp Glu Thr Leu 20 25 30

Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr Ile Ile Glu Ala Asp 35 40 45

Leu Ser His Leu Asn Val Arg His Leu Asp Leu Thr Phe Ser Gly Tyr 50 55 60

Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln Leu Tyr Glu Lys Ser 65 70 75 80
--

Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln Ile Glu Ala Glu Cys 85 90 95

Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys Glu Ser Ser Lys Asp 100 105 110
--

10295.204.ST25.txt

Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile Ser Asn Leu His Asn
115 120 125

Lys Gln Asn Pro Asp Ser Ala
130 135

<210> 182
<211> 2155
<212> DNA
<213> *Bacillus licheniformis*

<220>
 <221> CDS
 <222> (501)..(1655)

<400> 182	aaaggtttcc agaaagcttc ggcgtttctt ttgatgagct gatgacagcgc gccggctatg	60
	cgtggagaa gacgcaggaa agcgaacgtc cggatattca ctcgtcagtt gccgaaattg	120
	aagatgtttt gcaaacctca aatgtctatg atcggccatt taccatggaa gaactgaaaa	180
	acaaaattgaa tgagtgcgaa caatattctc agacggagga agaaaagcgt accattctgg	240
	ctgagttga atctaaaatc gagaaagttg ccggcattgg tcctttctg acccgctcgc	300
	acgacatgta cagcagattt acctcggggc gggggacgcc gcgtgaattt ctgctgatgg	360
	gcggcgctt gctgtatttc atcgttctg ttgatgtcat accggattat attttccga	420
	tcggctatat cgatgatgcg gcagcggttc atttcgaaaa caaccagctg tcatataaat	480
	catgatggag catgttcaag atg aaa aga aag cat atc aac att gac atc agt	533
	Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser	
	1 5 10	
	ctg ctg ctc att cta ttt tgt ttg ttt atc atc agc ctg ctg gcc gtt	581
	Leu Leu Leu Ile Leu Phe Cys Leu Phe Ile Ser Leu Leu Ala Val	
	15 20 25	
	tac agc ggg tcg ggc cag tat gaa aca cag gac cct ttt tat ttt gcc	629
	Tyr Ser Gly Ser Gly Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala	
	30 35 40	
	aaa cgg cag gtc ttt tgg tat ctt gtc ggg ttt ggc gtc atg gcg gga	677
	Lys Arg Gln Val Phe Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly	
	45 50 55	
	acg gcc tac atc gac tat gag ctg ctt gaa cga ttg gcg ctt cgt tta	725
	Thr Ala Tyr Ile Asp Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu	
	60 65 70 75	
	ttt gtg gga gcc gtt ttt ctt ctg att ctc gtt cat ttt ttt gga act	773
	Phe Val Gly Ala Val Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr	
	80 85 90	
	tac aaa aac ggt tcg caa agg tgg atc agc ttc ggg gtc atc gaa atc	821
	Tyr Lys Asn Gly Ser Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile	
	95 100 105	
	cag cct tca gaa ttt atg aag atc att ttg att ctt ctg ctg gct tcg	869
	Gln Pro Ser Glu Phe Met Lys Ile Ile Leu Ile Leu Leu Ala Ser	
	110 115 120	

10295.204.ST25.txt

ata ctc aat caa ttt cag cat aaa agg ttc tcc ttc gcc gag agc atc Ile Leu Asn Gln Phe Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile 125 130 135	917
att ccg acg gga aaa atc atg atg tac acg gtg att ccg ttt ttc ttt Ile Pro Thr Gly Lys Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe 140 145 150 155	965
ata ttg gtt cag cca gat tta ggg tcc gca ttg gtg att tta tcg atc Ile Leu Val Gln Pro Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile 160 165 170	1013
gca ttc acg ttg atg ctg gtc tcg ggg att tcg ggc agg atg atc gtg Ala Phe Thr Leu Met Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val 175 180 185	1061
tcc ctg tca ctt gga ttc atg gca ttg gtt gcc ttt ttg acg tat ttg Ser Leu Ser Leu Gly Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu 190 195 200	1109
cac aat cat tac ttt gag ata ttt tca aag att att aag cct cac cag His Asn His Tyr Phe Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln 205 210 215	1157
ctt gac cggttata tat ggc tgg ctc agt cct cat gaa cat gcc tct aca Leu Asp Arg Ile Tyr Gly Trp Leu Ser Pro His Glu His Ala Ser Thr 220 225 230 235	1205
tat gga tac cag ctg acg cag gcg tta ttg ggg atc gga tca ggc cag Tyr Gly Tyr Gln Leu Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln 240 245 250	1253
ctg tca ggg agc ggc ttt act caa gga atc caa gtt cag gga ggg aaa Leu Ser Gly Ser Gly Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys 255 260 265	1301
att ccg gag gct cat act gat ttt att ttc gcc gtg att ggt gag gaa Ile Pro Glu Ala His Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu 270 275 280	1349
ttc ggt ttt ttg ggt gcc gta aca tta gtc tgt ctg tat ttt ctg atg Phe Gly Phe Leu Gly Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met 285 290 295	1397
atc tac aga atc atc agg att gcg ctt tcg tcc aac agt ctg ttc ggt Ile Tyr Arg Ile Ile Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly 300 305 310 315	1445
ctt tat ata tgt gcg ggg gtt gca ggg ttg att gta ttc caa gtg ttc Leu Tyr Ile Cys Ala Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe 320 325 330	1493
caa aat atc ggg atg acg atc ggg tta atg ccg atc acg ggg ctc gct Gln Asn Ile Gly Met Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala 335 340 345	1541
ctt ccg ttt atc agc tat ggc ggc agc gcg ctg ttg acc aac atg atc Leu Pro Phe Ile Ser Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile 350 355 360	1589
gct tta ggt ctc gtt ttc agt gtg aat atc aga tct aaa cat tac atg Ala Leu Gly Leu Val Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met 365 370 375	1637
ttt ggg aat gat tgg gga tgaagttgct caaaaatgatt ctttccccatc Phe Gly Asn Asp Trp Gly 380 385	1685

10295,204.ST25.txt

taaagaaact tgattatgta ttgattgccg cggttctgtt tttatctgcg tttggcttgc	1745
tgatggata cagcgccggc taccccctcg gatatatgaa gtatcatgat ggcagctatt	1805
tttttatgaa gcagctgcaa tggctgctca tcggtttggc cttttttcg gctgccgcca	1865
ttttccata caaagcttac agcaaactca ttcggttttt ggtgaagctt tctttttaa	1925
tgctgattct cgttttgctg ccggaaatcg ggatggagaa aaacaattcc caaagggtgga	1985
ttcaattcgg ttcgctcatg attcagccgt ctgaggctgt gaagcttgc atggttattt	2045
atttcgcccta tgtgtatgca aaaaagcaga aatacatcgc cgatttcgga aaggcgtca	2105
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<210> 183
<211> 385
<212> PRT
<213> *Bacillus licheniformis*

<400> 183

Met Lys Arg Lys His ⁵Ile Asn ¹⁰Ile Asp ¹⁵Ile Ser Leu Leu Leu Ile Leu

Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val Tyr Ser Gly Ser Gly
20 25 30

Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala Lys Arg Gln Val Phe
35 40 45

Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly Thr Ala Tyr Ile Asp
50 55 60

Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu Phe Val Gly Ala Val
65 70 75 80

Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr Tyr Lys Asn Gly Ser
85 90 95

Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile Gln Pro Ser Glu Phe
100 105 110

Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser Ile Leu Asn Gln Phe
115 120 125

Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile Ile Pro Thr Gly Lys
130 135 140

Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe Ile Leu Val Gln Pro
145 150 155 160

Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile Ala Phe Thr Leu Met
165 170 175

10295.204.ST25.txt

Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val Ser Leu Ser Leu Gly
180 185 190

Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu His Asn His Tyr Phe
195 200 205

Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln Leu Asp Arg Ile Tyr
210 215 220

Gly Trp Leu Ser Pro His Glu His Ala Ser Thr Tyr Gly Tyr Gln Leu
225 230 235 240

Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln Leu Ser Gly Ser Gly
245 250 255

Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys Ile Pro Glu Ala His
260 265 270

Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu Phe Gly Phe Leu Gly
275 280 285

Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met Ile Tyr Arg Ile Ile
290 295 300

Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly Leu Tyr Ile Cys Ala
305 310 315 320

Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe Gln Asn Ile Gly Met
325 330 335

Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala Leu Pro Phe Ile Ser
340 345 350

Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile Ala Leu Gly Leu Val
355 360 365

Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met Phe Gly Asn Asp Trp
370 375 380

Gly
385

<210> 184
<211> 2113
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1613)

<400> 184

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cgtcgacg atcaaaaaca gactgtttt caatgacagc aaagcgacaa acattcttgc	120
gacgaaaaaa gcgctgtccg ccttcaaaa gccggtcatt ttgctggcag gggggcttga	180
ccgcggaaat gaatttgatg aactaaagcc gcatatgtct tttgtaaaag cggtgatcac	240
tttcggcgag accgcgccga agtttgagaa gctggccgaa gaaatgggaa tacaacagg	300
taaacgtgtc gataatgtt aacaaggcagc aactgcggcg ttcagcctgt cagacgaagg	360
agatgtcatt cttctgtccc cggcctgcgc aagctggat cagtacaaaa catttgaaga	420
acgtggtgac atgtttgtaa acgcccgtgca tatgctaaa taaggccttg tctcgtaaag	480
atagccctaa gaatttagagc ttg ggg tgt tcg gct ttg caa aca aaa aaa acg Leu Gly Cys Ser Ala Leu Gln Thr Lys Lys Thr	533
1 5 10	
tca ccg gat ttt ttg ctg gtt atc att acg cta ttg ctt tta aca atc Ser Pro Asp Phe Leu Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile	581
15 20 25	
gga ctg att atg gta tac agc gcc agt gca gta tgg gcg act tac aaa Gly Leu Ile Met Val Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys	629
30 35 40	
tac gac gac tcc ttt ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc Tyr Asp Asp Ser Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly	677
45 50 55	
atc ggg gtc atc gcc atg ttt ttc atc atg aac gtc gac tac tgg acg Ile Gly Val Ile Ala Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr	725
60 65 70 75	
tgg agg act tat gcg aaa ata ctg atc att gta tgt ttc ttt ctg ctc Trp Arg Thr Tyr Ala Lys Ile Leu Ile Val Cys Phe Phe Leu Leu	773
80 85 90	
atc atc gtc ctg gtt ccc ggg atc ggc atg gaa cgg aac ggg tcg agg Ile Ile Val Leu Val Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg	821
95 100 105	
agc tgg atc gga gtc ggc gct ttc agc att cag ccg tcc gag ttt atg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met	869
110 115 120	
aaa ctc gcg atg atc gca ttt ttg gcc aag ttt tta tct gaa aag caa Lys Leu Ala Met Ile Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln	917
125 130 135	
aag aat att acg tcg ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile	965
140 145 150 155	
gtc ttt tca gct ttt ctg atc atc atg cag cct gac ctc gga aca Val Phe Ser Ala Phe Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr	1013
160 165 170	
gga acc gtg atg gtc ggc aca tgc atc att atg atc ttt gtc gcg ggg Gly Thr Val Met Val Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly	1061
175 180 185	
gcg aga att tcg cac ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt Ala Arg Ile Ser His Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly	1109
190 195 200	

10295.204.ST25.txt

ttt gtc ggc ctt gtg ctg tcg gcg ccg tac cg _g atc aaa agg atc act Phe Val Gly Leu Val Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr 205	210	215	1157	
tca tac ttg aac cct tgg gag gac cct tta gga agc ggc ttt caa atc Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile 220	225	230	235	1205
att cag tct ctt tat gc _g gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly Leu Phe Gly Leu Gly 240	245	250		1253
ctc ggc cag agc agg caa aag ttt ttc tat ctg cct gag cc _g cag aca Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr 255	260	265		1301
gat ttt att ttt gc _g att tta tca gag gag ctc ggc ttt atc ggc gga Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly 270	275	280		1349
tcg ctg att ctt ttg ctc ttc agc gtt cta tta tgg aga ggc atc aga Ser Leu Ile Leu Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg 285	290	295		1397
atc gc _g ctc ggt gc _g ccc gat tta tac ggc agt ttt gtc gcc gtc ggc Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly 300	305	310	315	1445
gtc att tcg atg ata gc _g att cag gtt atg atc aat atc gga gtc gtq Val Ile Ser Met Ile Ala Ile Gln Val Met Ile Asn Ile Gly Val Val 320	325	330		1493
act ggt ttg att cct gtt aca ggc att acg ctt cc _g ttt tta agc tat Thr Gly Leu Ile Pro Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr 335	340	345		1541
ggc ggt tca tca ctg acc ttg atg ctc atg gc _g gtc ggc gt _g ctg ctg Gly Gly Ser Ser Leu Thr Leu Met Leu Met Ala Val Gly Val Leu Leu 350	355	360		1589
aat gtc agc agg tat tct aga tac tagat _{ttt} gg cgataaccct gttgcgagat Asn Val Ser Arg Tyr Ser Arg Tyr 365	370			1643
agcagggtta tcggcgtgta cataaggatt aaggggaga acagatgcgg attgttgtta				1703
gcggaggcgg aacgggcggc catatttacc cccccc _{tt} gc gtttattaaa gaagtgaaac				1763
ggcatcacga agatgttgag ttttatata tcggaccga aaaaggcctg gagaaaaata				1823
tcgtcgagcg ggaagggatc ctttcaaag cgattgaaat tacgggtttt aaaagaaaac				1883
tttcatttga aaacgtcaaa accgtcatgc gcttttaaa gggtgtaaaa gaatgcaaag				1943
aagaattaaa acggttcaag ccggatgccg tgatccgcac gggcggctac gtgtcggcc				2003
ccgtcgata cggcgttca aaactgggaa ttccgacgat tatccacgaa caaaacagcc				2063
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<210> 185
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<212> PRT
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<400> 185

10295.204.ST25.txt

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Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val
20 25 30

Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
35 40 45

Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
50 55 60

Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
65 70 75 80

Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
85 90 95

Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
100 105 110

Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
115 120 125

Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
130 135 140

Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
145 150 155 160

Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
165 170 175

Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
180 185 190

Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
195 200 205

Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
210 215 220

Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
225 230 235 240

Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
245 250 255

Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
260 265 270

10295.204.ST25.txt
 Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
 275 280 285

Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
 290 295 300

Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
 305 310 315 320

Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
 325 330 335

Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
 340 345 350

Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
 355 360 365

Ser Arg Tyr
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<211> 2040
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501)..(1976)

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	aaggcgacat taaaagtggat taccggatgg atttggccaa gctgatgaag aagtcgaaaa	180
	aaacggtaaa gccgggcgag gaagtccaag atttgatgtg ggaagagacg ccttcgttc	240
	cggcgcccc ggtaaagtac acagtgaatg acaaacagga acctgtttt ctcgaataga	300
	atatcggtca aaatgcaagt atcagtcatg aacctttctc ctcggcatac aatgaggaga	360
	aaggttttt catgtatgcc gaaaaaattt ccctaagctg tcataattgaa ataggacaac	420
	gtcatacact atagtgtcct gttttgatt gatgaagaag taaaaaattt aaaaaggattt	480
	gaagtccggg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct	533
	Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala	
	1 5 10	

gaa cga aca gga ggc gat ata tac tta ggt gtc gta gga gct gta cgt	581
Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg	
15 20 25	

aca gga aaa tct acg ttt atc aaa aaa ttt atg gag cta gtg gtg ctc	629
Thr Gly Lys Ser Thr Phe Ile Lys Phe Met Glu Leu Val Val Leu	
30 35 40	

ccg aat atc aac aat gaa gca gac cgg gcg cgc gca caa gat gag ctc	677
Page 279	

10295.204.ST25.txt

Pro Asn Ile Asn Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu	45 50 55	
ccc caa agt gcc gct ggc aaa acc att atg aca act gaa ccg aag ttt		725
Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe	60 65 70 75	
gtt ccg aat cag gca atg tca gtt cat gtc agt gac gga ctc gat gtg		773
Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val	80 85 90	
aat ata agg ctt gtc gac tgc gtc ggc tat act gta ccc ggg gca aag		821
Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys	95 100 105	
gga tac gag gat gaa aac ggg ccg aga atg atc aat act cct tgg tat		869
Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr	110 115 120	
gaa gag ccg att ccg ttt cac gaa gct gcc gaa atc ggc acg aga aaa		917
Glu Glu Pro Ile Pro Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys	125 130 135	
gtc atc caa gag cac tcc aca atc ggt gtt gtg att acg act gac ggc		965
Val Ile Gln Glu His Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly	140 145 150 155	
acg att gga gaa atc gcc aga cag gat tat gtc gag gct gaa gaa cgg		1013
Thr Ile Gly Glu Ile Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg	160 165 170	
gtg atc gac gag ttg aaa gag gtt gga aaa ccg ttt atc atg gtc atc		1061
Val Ile Asp Glu Leu Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile	175 180 185	
aat tcc gta agg ccg tat cat ccg gaa aca gaa gcg ctc agg caa gaa		1109
Asn Ser Val Arg Pro Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu	190 195 200	
ttg atg gaa aag tac gac att ccg gtg ctg gcg atg agc gtt gaa agc		1157
Leu Met Glu Lys Tyr Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser	205 210 215	
atg agg gaa gcg gac gtt ctg agc gtt ctc aga gaa gcg ctt tac gaa		1205
Met Arg Glu Ala Asp Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu	220 225 230 235	
tcc cct gtg ctc gaa gtc aac gtc aat ctt cca agc tgg gtg atg gta		1253
Phe Pro Val Leu Glu Val Asn Val Asn Leu Pro Ser Trp Val Met Val	240 245 250	
tta aaa gag aat cat tgg ctc agg gaa aac tat caa gat tcc gtt aaa		1301
Leu Lys Glu Asn His Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys	255 260 265	
gaa acc gtc aaa gat att aaa aga ctg aga gat gtc gac cgc gtc gtc		1349
Glu Thr Val Lys Asp Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val	270 275 280	
gga cac ttc agc gaa ttt gat ttc atc gag cgc gca agc ctc gcc gga		1397
Gly His Phe Ser Glu Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly	285 290 295	
att gaa atg ggc cag ggg atc gcg gaa atc gat tta tac gcg ccg gat		1445
Ile Glu Met Gly Gln Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp	300 305 310 315	
		1493
tac ctg tac gat gaa att ttg agg gaa gtc gtc ggc gtt gaa atc aga		

10295.204.ST25.txt

Tyr Leu Tyr Asp Glu Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg
 320 325 330

gga aaa gat cac ctc ctt cag ctc atg cag gat ttt gcc cat gcc aag 1541
 Gly Lys Asp His Leu Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys
 335 340 345

acc gaa tat gat caa gtc tca gat gca ttg aaa atg gtg aaa caa acc 1589
 Thr Glu Tyr Asp Gln Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr
 350 355 360

ggc tat gga atc gca gct ccc gca tta acc gat atg agc ctg gat gaa 1637
 Gly Tyr Gly Ile Ala Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu
 365 370 375

ccg gaa atc atc agg cag ggt tca aga ttc gga gtc cg^g ctg aag gcg 1685
 Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala
 380 385 390 395

gtg gcg ccg tcg att cat atg atc aaa gtc gat gtg gaa agc gag ttt 1733
 Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe
 400 405 410

g^cg ccg atc atc gga aca gag aag cag agc gaa gag ctt gtc cgc tat 1781
 Ala Pro Ile Ile Gln Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr
 415 420 425

tta atg cag gac ttt gag gac gat ccg ctg tca atc tgg aat tcc gac 1829
 Leu Met Gln Asp Phe Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp
 430 435 440

ata ttc gga aga agc ttg agc tcg atc gtc aga gaa ggg att cag gcg 1877
 Ile Phe Gln Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala
 445 450 455

aag ctg tca ctc atg cct gaa aat gcg aga tat aag ctg aag gag acg 1925
 Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr
 460 465 470 475

ctg gag cgc att atc aat gaa ggc tca ggc ggc ttg att gcg atc atc 1973
 Leu Glu Arg Ile Ile Asn Glu Gln Ser Gly Gly Leu Ile Ala Ile Ile
 480 485 490

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 Leu

acaggctgaa cggg 2040

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<213> Bacillus licheniformis

<400> 187

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 20 25 30

Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Asn Asn
 35 40 45

10295.204.ST25.txt

Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala
50 55 60

Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala
65 70 75 80

Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val
85 90 95

Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu
100 105 110

Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro
115 120 125

Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His
130 135 140

Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Glu Ile
145 150 155 160

Ala Arg Gln Asp Tyr Val Glu Ala Glu Glu Arg Val Ile Asp Glu Leu
165 170 175

Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro
180 185 190

Tyr His Pro Glu Thr Glu Ala Leu Arg Gln Glu Leu Met Glu Lys Tyr
195 200 205

Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ala Asp
210 215 220

Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu
225 230 235 240

Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His
245 250 255

Trp Leu Arg Glu Asn Tyr Gln Asp Ser Val Lys Glu Thr Val Lys Asp
260 265 270

Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly His Phe Ser Glu
275 280 285

Phe Asp Phe Ile Glu Arg Ala Ser Leu Ala Gly Ile Glu Met Gly Gln
290 295 300

Gly Ile Ala Glu Ile Asp Leu Tyr Ala Pro Asp Tyr Leu Tyr Asp Glu
305 310 315 320

10295.204.ST25.txt

Ile Leu Arg Glu Val Val Gly Val Glu Ile Arg Gly Lys Asp His Leu
 325 330 335

Leu Gln Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln
 340 345 350

Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala
 355 360 365

Ala Pro Ala Leu Thr Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg
 370 375 380

Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile
 385 390 395 400

His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly
 405 410 415

Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe
 420 425 430

Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser
 435 440 445

Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met
 450 455 460

Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr Leu Glu Arg Ile Ile
 465 470 475 480

Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile Leu
 485 490

<210> 188
 <211> 5482
 <212> DNA
 <213> *Bacillus licheniformis*

<220>
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 <222> (501)..(4982)

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gacgcggcgc caataaagaa gcgcttgaga cggcccgtaa gctggaaaac aatgcacaga	180
tcatgttggc acttatgaaa tacacagatg acattaaagc cgatgataaa ttgtccagtg	240
atgagcggca gaaacagctg gatccgctcg aaaaagaact tgaagaattg aagcggacag	300
cggatgaaca gaaagccaaa actgaagaaa accagcaggc aaacaccgag caaaaccagg	360

10295.204.ST25.txt

cgacgtaga ggccgcaaag gctgaaacgg agaaggccga gaaggaacag gcgaaaaaag	420
aaaataaaga aaaggaagac aaaaagaaaa aagatgacaa ataaaagcga aaacacctgt	480
tgttggcagg aggccggagaa atg agt ctg tta tgg att ttt tat cat aaa aac Met Ser Leu Leu Trp Ile Phe Tyr His Lys Asn	533
1 5 10	
tat caa aaa ata aaa ctg gat gat cag aac agc cgc acg ctc acc atc Tyr Gln Lys Ile Lys Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile	581
15 20 25	
ggg ccg gat ttg aaa cat tct gtc acg att aag cat ttt tca ttt gaa Gly Pro Asp Leu Lys His Ser Val Thr Ile Lys His Phe Ser Phe Glu	629
30 35 40	
aaa ggc ccg gtg aca ctg gaa aag cag aag gac tca gac gct ttg aac Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn	677
45 50 55	
gtg cag ctg gga ggg gag acg gtc tct tct tta aag ctt ggc gga aag Val Gln Leu Gly Gly Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys	725
60 65 70 75	
gcg tcc gtc caa agc ggc gct gaa cag ctg acg ctc ttt tta gcc gaa Ala Ser Val Gln Ser Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu	773
80 85 90	
gaa gcc gac agc gtt cct gcc tac tat ttg gga gag aga cag gaa atc Glu Ala Asp Ser Val Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile	821
95 100 105	
gtc att tct tcc ctc gat caa gaa gcg gat gtt tat ttc aat gaa acg Val Ile Ser Ser Leu Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr	869
110 115 120	
gat tca ttc ttt gga gaa aaa ggt acg ttc tct ttc atc cgc ctc gac Asp Ser Phe Phe Gly Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp	917
125 130 135	
ggg caa tgg aat gtc ctg ccg aat gac gcg aaa att tat ttg aac gga Gly Gln Trp Asn Val Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly	965
140 145 150 155	
gaa gaa gtg tcc gcc cct gtc tcc gtg caa aat gga gac gaa atc gca Glu Glu Val Ser Ala Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala	1013
160 165 170	
ttt gga ctg aat att ctt cgc atc gtt gaa gac gac ctc ttg gaa atc Phe Gly Leu Asn Ile Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile	1061
175 180 185	
gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro	1109
190 195 200	
agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg	1157
205 210 215	
atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala	1205
220 225 230 235	
cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro	1253
240 245 250	

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ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro 255 260 265	1301
cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu 270 275 280	1349
att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys 285 290 295	1397
aga gaa gaa aaa aga gag cggtt gtc tat acc ctt tac ctt gaa aac aaa Arg Glu Glu Lys Arg Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys 300 305 310 315	1445
aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp 320 325 330	1493
ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile 335 340 345	1541
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln 350 355 360	1589
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu 365 370 375	1637
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln 380 385 390 395	1685
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile 400 405 410	1733
act gtg aat ctt gcc gaa ggc ccg atg ggc gtc gtc gga aaa ttg tcc Thr Val Asn Leu Ala Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser 415 420 425	1781
gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe 430 435 440	1829
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu 445 450 455	1877
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro 460 465 470 475	1925
cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln 480 485 490	1973
ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu 495 500 505	2021
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr 510 515 520	2069

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aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly 525 530 535	2117
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys 540 545 550 555	2165
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu 560 565 570	2213
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro 575 580 585	2261
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc cgg Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg 590 595 600	2309
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro 605 610 615	2357
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp 620 625 630 635	2405
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu 640 645 650	2453
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn 655 660 665	2501
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr 670 675 680	2549
ggg tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597
gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys 700 705 710 715	2645
ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly 720 725 730	2693
acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu 735 740 745	2741
gag tcc att aag agc gag ctg aag aaa agg cag cgg ctc ttt gat gag Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln 750 755 760	2789
tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa gag aaa Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys 765 770 775	2837
aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe 780 785 790 795	2885

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gcc gag ctg aaa agc gaa gaa	ccg gaa ttt atc cgc gag ctt	gtc agt	2933
Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser			
800	805	810	
gca gca agg atc ggg cga agc	ctc ggg gtg cac tta atc ttg	gca acg	2981
Ala Ala Arg Ile Gly Arg Ser	Leu Gly Val His Leu Ile Leu Ala Thr		
815	820	825	
caa aaa ccg ggc ggc atc atc	gat gac cag att tgg	agc aac tcc aga	3029
Gln Lys Pro Gly Gly Ile Ile	Asp Asp Gln Ile Trp Ser Asn Ser Arg		
830	835	840	
ttc aag gtc gcc ttg aag	gtg cag gat gcg aat gac	agt aaa gag atc	3077
Phe Lys Val Ala Leu Lys	Val Gln Asp Ala Asn Asp Ser Lys Glu Ile		
845	850	855	
ctc aaa aac ggg gat gcg	gct acc atc acg gta acg	ggc cgc ggc tat	3125
Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val	Thr Val Gln Arg Gly Tyr		
860	865	870	875
ttg caa gtc ggc aac aac	gag gtg tat gaa ctg ttc cag tct	gca tgg	3173
Leu Gln Val Gly Asn Asn Glu Val Tyr	Glu Leu Phe Gln Ser Ala Trp		
880	885	890	
agc gga gcc cct tac atg	gag gac ggc tac ggc aca	gag gat gaa gtg	3221
Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val			
895	900	905	
gcg atc gtc aca gat acc	gga tta att cct tta tca	gat gtt gat gct	3269
Ala Ile Val Thr Asp Thr Gly	Ile Pro Leu Ser Asp Val Asp Ala		
910	915	920	
gat cgc gct gcg aaa aaa	gag gct gtg acg gaa att tcg	gca gtc gtc	3317
Asp Arg Ala Ala Lys Lys	Glu Ala Val Thr Glu Ile Ser Ala Val Val		
925	930	935	
gaa caa att gaa cgg att	caa gcg gag atg gga atc	gag aag ctc ccg	3365
Glu Gln Ile Glu Arg Ile	Gln Ala Glu Met Gly Ile Glu Lys Leu Pro		
940	945	950	955
agc cct tgg ctg ccg	ccg ctt gaa gaa cgc ata ccg	aaa acg cgc tat	3413
Ser Pro Trp Leu Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr			
960	965	970	
ccg tcg gag gaa gcc gat	gcc ttt aac ttt gcc tat atc	gat gaa cct	3461
Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro			
975	980	985	
gaa aag caa agc cag	gag ccg atc agc tac cgc atg	atg gaa gac ggc	3509
Glu Lys Gln Ser Gln Glu Pro Ile Ser Tyr Arg Met			
990	995	1000	
aat atc ggc atc gtc ggc	tcg tca ggc tac gga aaa	tcc ctg aca	3554
Asn Ile Gly Ile Val Gly	Ser Ser Gly Tyr Gly Lys Ser Leu Thr		
1005	1010	1015	
gcc acg acg ttc atg atg	agc ttt gcc gaa cag tat	acg ccg gaa	3599
Ala Thr Thr Phe Met Met	Ser Phe Ala Glu Gln Tyr	Thr Pro Glu	
1020	1025	1030	
gaa ttg cat tac tac att	ttc gac ttt ggc aac gga	acg ctg ctt	3644
Glu Leu His Tyr Tyr Ile	Phe Asp Phe Gly Asn Gly	Thr Leu Leu	
1035	1040	1045	
ccg ctt gca agg ctt ccg cac	acc gcg gat tat ttc	ctg atg gac	3689
Pro Leu Ala Arg Leu Pro His	Thr Ala Asp Tyr Phe	Leu Met Asp	
1050	1055	1060	

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caa acg	aga aaa atc	gag aaa	ttt atg gtc	cg ^g atc	aag gc ^g	gaa	3734
Gln Thr	Arg Lys Ile	Glu Lys	Phe Met Val	Arg Ile	Lys Ala	Glu	
1065	1070		1075				
atc gag	cac agg aaa aat	ctc	t ^t c cgt gca	aaa gaa	atc agc	cat	3779
Ile Glu	His Arg Lys Asn	Leu	Phe Arg Ala	Lys Glu	Ile Ser	His	
1080	1085		1090				
atc aag	atg tac aat	gc ^g ctg	aat gag gaa	aag ctg	ccg ttt	att	3824
Ile Lys	Met Tyr Asn Ala	Leu	Asn Glu Glu	Lys Leu	Pro Phe	Ile	
1095	1100		1105				
t ^t c ata	acg gtc gac aac	t ^t t phe	gac atc att	aaa gac	gaa atg	cat	3869
Phe Ile	Thr Val Asp Asn		Asp Ile Ile	Lys Asp	Glu Met	His	
1110	1115		1120				
gaa ctc	gaa agc gaa ttt	atc	cag ttt tca	cg ^g gac	ggc cag	tcg	3914
Glu Leu	Glu Ser Glu Phe	Ile	Gln Phe Ser Arg	Asp Asp	Gly Gln	Ser	
1125	1130		1135				
ctt gga	att tat tta atc	ctg	acc gcg aca	agg gtc	aat gca	atc	3959
Leu Gly	Ile Tyr Leu Ile	Leu	Thr Ala Thr Arg	Val	Asn Ala	Ile	
1140	1145		1150				
aga cag	tcg ctc ttg aac	aac	ctg aaa acg	agg gtt	gtc cac	tat	4004
Arg Gln	Ser Leu Leu Asn	Asn	Leu Lys Thr Arg	Val	Val His	Tyr	
1155	1160		1165				
ctg atg	gat cag tct gaa	gca	tat tcg att	atc gga	agg ccg	gaa	4049
Leu Met	Asp Gln Ser Glu	Ala	Tyr Ser Ile Ile	Gly	Arg Pro	Glu	
1170	1175		1180				
t ^t c agc	ctt gaa cc ^g atc	cct	gga cg ^g gtt	att atc	aat aaa	gaa	4094
Phe Ser	Leu Glu Pro Ile	Pro	Gly Arg Val	Ile Ile	Asn Lys	Glu	
1185	1190		1195				
aac caa	tac ttc gca caa	atg	t ^t t atg cct	gtg gaa	g ^c g gac	aac	4139
Asn Gln	Tyr Phe Ala Gln	Met	Phe Met Pro Val	Glu	Ala Asp	Asn	
1200	1205		1210				
gat atc	gag ctg ttt gaa	ggg	atc aaa gcc	gac att	cag g ^c g	atc	4184
Asp Ile	Glu Leu Phe Glu	Gly	Ile Lys Ala Asp	Ile	Gln Ala	Ile	
1215	1220		1225				
gca gaa	cgc tcg gaa ggc	atg	aga aag cc ^g	g ^c g cct	gtg ccg	atg	4229
Ala Glu	Arg Ser Glu Gly	Met	Arg Lys Pro Ala	Pro	Val Pro	Met	
1230	1235		1240				
ctg cc ^g	ctc gag ctt tcc	g ^t c	aca cag ttt gtg	aga	gat tat	cc ^g	4274
Leu Pro	Leu Glu Leu Ser	Val	Thr Gln Phe Val	Arg	Asp Tyr	Pro	
1245	1250		1255				
ctt cag	cct gaa aga ggc	ctt	att cca atg gga	ctc	gat gaa	gaa	4319
Leu Gln	Pro Glu Arg Gly	Leu	Ile Pro Met Gly	Leu	Asp Glu	Glu	
1260	1265		1270				
act gtc	gaa ccc gta tac	t ^t t	aat ctt gag aaa	aat	aag cac	tgc	4364
Thr Val	Glu Pro Val Tyr	Phe	Asn Leu Glu Lys	Asn	Lys His	Cys	
1275	1280		1285				
ctc att	atg ggt cag acg	cag	cg ^g gga aaa	aca aac	gtc atc	aag	4409
Leu Ile	Met Gly Gln Thr	Gln	Arg Gly Lys Thr	Asn	Val Ile	Lys	
1290	1295		1300				
atc atg	ctc gag cac ctg	ctt	gac cat gac acg	aaa	aaa atc	gcc	4454
Ile Met	Leu Glu His Leu	Leu	Asp His Asp Thr	Lys	Lys Ile	Ala	
1305	1310		1315				

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gtg ttt gat tcg ata gac aga	1320	ggg ctt tct caa tat	1325	gcy aca gag	1330	4499
Val Phe Asp Ser Ile Asp Arg		Gly Leu Ser Gln Tyr		Ala Thr Glu		
gat caa atc agc tat cta gaa	1335	aca aaa gac gac att	1340	ctg ctc tgg	1345	4544
Asp Gln Ile Ser Tyr Leu Glu		Thr Lys Asp Asp Ile		Leu Leu Trp		
ctc gct gag acg gaa gaa att	1350	tgc cgg aca agg gaa	1355	gcy atg tat	1360	4589
Leu Ala Glu Thr Glu Glu Ile		Cys Arg Thr Arg Glu		Ala Met Tyr		
ttg gaa gcc gtt aaa caa gga	1365	gaa atc gcc aac ctt	1370	gat ttc tca	1375	4634
Leu Glu Ala Val Lys Gln Gly		Gl Glu Ile Ala Asn Leu		Asp Phe Ser		
ccg atg gtc ttt att gtc gac	1380	gga att tca cggttc	1385	cag cag acg	1390	4679
Pro Met Val Phe Ile Val Asp		Gly Ile Ser Arg Phe		Gln Gln Thr		
atc gac gca tcg att cag gac	1395	aaa atg gcg atg ttc	1400	atg aaa tct	1405	4724
Ile Asp Ala Ser Ile Gln Asp		Lys Met Ala Met Phe		Met Lys Ser		
tac gcc cat tta ggt ttc cac	1410	ttt ata cct gcc gga	1415	aat cac agc	1420	4769
Tyr Ala His Leu Gly Phe His		Phe Ile Pro Ala Gly		Asn His Ser		
gag ttc aca aaa ggc tat gat	1425	tcg ctg aca agc gaa	1430	gtc aag cag	1435	4814
Gl Glu Phe Thr Lys Gly Tyr		Ser Leu Thr Ser Glu		Val Lys Gln		
gtc aga cac gcg atg cta ttg	1440	atg aaa aaa tcc gag	1445	cag aac ttg	1450	4859
Val Arg His Ala Met Leu Leu		Met Lys Lys Ser Glu		Gln Asn Leu		
att cag ctc cca tat gaa cgc	1455	cag gag ccg gaa att	1460	ctg ccg ggc	1465	4904
Ile Gln Leu Pro Tyr Glu Arg		Gln Glu Pro Glu Ile		Leu Pro Gly		
ttt ggc tat atc gtt gaa aac	1470	ggc aaa gag agg aaa	1475	att caa att	1480	4949
Phe Gly Tyr Ile Val Glu Asn		Gly Lys Glu Arg Lys		Ile Gln Ile		
cct tta tgt gct gta gaa agg	1485	aag aaa gcg aaa tgacggaca	1490			4992
Pro Leu Cys Ala Val Glu Arg		Lys Lys Ala Lys				
aaaaaaaaagc acgctaaaaa ttatcagcgc catcgtaacg atcatcttc tgcccgctc						5052
gtttttcat ttcatcggtg agaacccgac gaaaaaggta tcgaacgcga caagggaaat						5112
cggcggtgtc aatgaggata cccgggtttt gaaagatgac ggaaccgttg atcaagatgc						5172
gctgctggaa aacgaaatct cggctccct gggtgaccgt ccggattata aatggacggt						5232
cgtcaaccgg agcgcagcag aaagcggact tgcggagaag caatacgatg cgattgtcta						5292
cattccgtcg gactttcgc aaaacatttt aagctacaac catgagcgtc cgcaaaaagc						5352
ggagctggaa ttcaaaattc aggaccagct cgacgccgtc aacaaggaaa aagtccagcg						5412
cgagcttcag gacgcgcaa aaacggtgag caagaaaatg tcttccctgt actggcgctt						5472
tgtcaaacag						5482

10295.204.ST25.txt

<211> 1494
<212> PRT
<213> *Bacillus licheniformis*

<400> 189

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1 5 10 15

Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile Gly Pro Asp Leu Lys
20 25 30

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
35 40 45

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
50 55 60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
65 70 75 80

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
85 90 95

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
100 105 110

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
115 120 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
130 135 140

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
145 150 155 160

Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
165 170 175

Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
180 185 190

Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
195 200 205

Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
210 215 220

Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
245 250 255

10295.204.ST25.txt

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
290 295 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
385 390 395 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
420 425 430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
435 440 445

Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Thr
500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
515 520 525

10295.204.ST25.txt

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
530 535 540

Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Met Ala
705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
785 790 795 800

10295.204.ST25.txt

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
805 810 815

Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
820 825 830

Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
835 840 845

Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
850 855 860

Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
865 870 875 880

Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
885 890 895

Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
900 905 910

Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
915 920 925

Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
930 935 940

Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
945 950 955 960

Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
965 970 975

Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
980 985 990

Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
995 1000 1005

Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
1010 1015 1020

Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu Glu Leu His Tyr Tyr
1025 1030 1035

Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
1040 1045 1050

Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile
1055 1060 1065

10295.204.ST25.txt

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Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
1085 1090 1095

Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
1100 1105 1110

Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
1115 1120 1125

Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
1130 1135 1140

Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
1145 1150 1155

Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
1160 1165 1170

Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
1175 1180 1185

Ile Pro Gly Arg Val Ile Ile Asn Lys Glu Asn Gln Tyr Phe Ala
1190 1195 1200

Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
1205 1210 1215

Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu
1220 1225 1230

Gly Met Arg Lys Pro Ala Pro Val Pro Met Leu Pro Leu Glu Leu
1235 1240 1245

Ser Val Thr Gln Phe Val Arg Asp Tyr Pro Leu Gln Pro Glu Arg
1250 1255 1260

Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
1265 1270 1275

Tyr Phe Asn Leu Glu Lys Asn Lys His Cys Leu Ile Met Gly Gln
1280 1285 1290

Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
1295 1300 1305

Leu Leu Asp His Asp Thr Lys Lys Ile Ala Val Phe Asp Ser Ile
1310 1315 1320

10295.204.ST25.txt

Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu Asp Gln Ile Ser Tyr
1325 1330 1335

Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
1340 1345 1350

Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
1355 1360 1365

Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
1370 1375 1380

Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
1385 1390 1395

Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
1400 1405 1410

Phe His Phe Ile Pro Ala Gly Asn His Ser Glu Phe Thr Lys Gly
1415 1420 1425

Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met
1430 1435 1440

Leu Leu Met Lys Lys Ser Glu Gln Asn Leu Ile Gln Leu Pro Tyr
1445 1450 1455

Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly Phe Gly Tyr Ile Val
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Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile Pro Leu Cys Ala Val
1475 1480 1485

Glu Arg Lys Lys Ala Lys
1490

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<211> 3343
<212> DNA
<213> *Bacillus licheniformis*

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<222> (501)..(2843)

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gaatataatc gaacaaaaca aggacgcaca ggaagggata atccaatgat tctgtatacg	180
aaaatgccgc aggaaatcgt gttcgcaggg caggcgaaaa actcgaaatt aaaacagatc	240

10295.204.ST25.txt

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gttctcagca cgaacccgat ggattttta aaacaagaaa cggccctgg gcagacgctt	360
aaactgacat ttataaaata gctggagtgt ctcaaggata aatatgctat aatagggaa	420
tccagaggaa aatcgagcc gaaaaaaggc tgcttctct ttgttttac atttttaac	480
acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys	533
1 5 10	
caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly	581
15 20 25	
tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val	629
30 35 40	
gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp	677
45 50 55	
ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe	725
60 65 70 75	
tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu	773
80 85 90	
tac tgc atc att gca agc atg ctg ctt tca cat gtc cag ctg ttt Tyr Cys Ile Ile Ala Ser Met Leu Leu Ser His Val Gln Leu Phe	821
95 100 105	
cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln	869
110 115 120	
aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser	917
125 130 135	
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca Pro Asp Leu Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser	965
140 145 150 155	
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160 165 170	
atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg Ile Leu Ile Gly Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr	1061
175 180 185	
ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp	1109
190 195 200	
cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys	1157
205 210 215	
aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser	1205
220 225 230 235	

10295.204.ST25.txt

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln 240 245 250	1253
tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu 255 260 265	1301
gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu 270 275 280	1349
ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr 285 290 295	1397
ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu 300 305 310 315	1445
ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile 320 325 330	1493
tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val 335 340 345	1541
aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr 350 355 360	1589
gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu 365 370 375	1637
agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa Ser Asp Asp Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu 380 385 390 395	1685
gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtc ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 400 405 410	1733
gaa gtg gcg atg gtt tcc ttg aaa gaa gtc ctt gaa tcg aaa ctg aat Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn 415 420 425	1781
gac ccg ccg gat gca aag ctg atg atc ggc ctc ggc cgg aac att tcc Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser 430 435 440	1829
gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val 445 450 455	1877
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475	1925
aca agc att ttg atg agg gca aag ccc cac gaa gtc aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490	1973
att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His 495 500 505	2021

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ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu 510 515 520	2069
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acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met 540 545 550 555	2165
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att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val 575 580 585	2261
gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile 590 595 600	2309
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly 605 610 615	2357
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser 620 625 630 635	2405
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu 640 645 650	2453
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro 655 660 665	2501
ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val 670 675 680	2549
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tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val 720 725 730	2693
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg ccg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745	2741
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly 750 755 760	2789
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu 765 770 775	2837

10295.204.ST25.txt

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<212> PRT

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20	25	30	
30			

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe			
35	40	45	
45			

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu			
50	55	60	
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Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Thr			
65	70	75	80
75	80		

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala			
85	90	95	
95			

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu			
100	105	110	
110			

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu			
115	120	125	
125			

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly			
130	135	140	
140			

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala			
145	150	155	160
155	160		

10295.204.ST25.txt

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
180 185 190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

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Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
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450 455 460

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465 470 475 480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
485 490 495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
500 505 510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
515 520 525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
530 535 540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545 550 555 560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
565 570 575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
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Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
595 600 605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
610 615 620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
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Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
645 650 655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
660 665 670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
675 680 685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
690 695 700

10295.204.ST25.txt

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780